

SEQUENCE LISTING

#24/E

<110> Kauppinen, Markus  
Schulein, Martin  
Schnorr, Kirk  
Andersen, Lene  
Bjornvad, Mads

<120> Novel Mannanases

<130> 5440.204-US

<160> 55

<170> PatentIn version 3.1

<210> 1

<211> 1470

<212> DNA

<213> Bacillus sp. I633

<400> 1

|  |      |
|--|------|
| ttgaataatg gttttaaaaa aattttttct ataacattat cattactatt agctagctct  | 60   |
| attctgttcg ttccaggaac ttctacagct aatgcaaatt ccggatttta tgtaagcggg  | 120  |
| accactctat acgatgccaa tggaaaccca ttgtaatga gagggattaa ccatgggcac   | 180  |
| gcatggtata aagaccaggc aactactgca attgaaggga ttgcaaatac cggtgcta    | 240  |
| acgggccgga ttgtgttatc tgatggggga caatggacaa aagatgacat ccatacagta  | 300  |
| agaaacctta tctcttttagc ggaagataat catttggttg ctgttcttga agttcatgat | 360  |
| gctaccgggt atgattccat tgcttcgctc aatcgtgctg ttgattattg gattgaaatg  | 420  |
| agaagtgcct taattggaaa ggaagatacc gtcattatta atattgcaa tgaatggttt   | 480  |
| ggttcgtggg aaggggatgc ttgggctgac gggataaac aagcaatccc gcgattgcgt   | 540  |
| aacgccggtc taaaccatac cttgatggta gatgctgcgg ggtggggaca atttccacaa  | 600  |
| tcgattcatg attatggaag agaagttttt aatgctgacc ctcaacgaaa tacaatgttt  | 660  |
| tcgattcata tgtatgaata tgcagggtgt aatgcatcgc aagttcgtac taatattgac  | 720  |
| cgagttctta atcaagacct cgcattagtc attggtgaat ttggacaccg tcatacaaat  | 780  |
| ggtgacgtcg atgaagcaac gattatgagc tattctgaac aaagaggagt tgggtggttg  | 840  |
| gcgtggtcat ggaaagggaa cggcccagaa tgggagtatt tagaccttc gaatgattgg   | 900  |
| gctggaaata accttacagc ttggggaaat acaatagtga atggtccata tggtttaaga  | 960  |
| gaaacttcga gattaagcac cgtttttaca ggtggaggat ctgatggagg aacttctccg  | 1020 |
| acaactcttt atgattttga aggtagtatg caaggatgga ctggaagtag cttgagcggg  | 1080 |

208

E

ggtccttggg ctgtgacaga gtggtcttct aaaggaagtc attctttaaa agcggatatt 1140  
 caattgtcgt caaattcaca acattactta catgttattc aaaatacgtc tttacagcag 1200  
 aatagtagga tacaagctac tggttaaacat gcaaattggg gaagtgttgg taatggaatg 1260  
 actgcgcgtc tttatgtgaa aacaggacat ggttatacat ggtactctgg aagctttgtg 1320  
 ccgattaacg gttcatctgg aacaacgcta tctctagatt tatcaaatgt ccaaaatctt 1380  
 tctcaagtaa gggaaattgg agttcagttc caatcagcga gtgatagtag tggacaaaca 1440  
 tcgatttata ttgataatgt gattgtagaa 1470

<210> 2  
 <211> 490  
 <212> PRT  
 <213> Bacillus

<400> 2

Leu Asn Asn Gly Phe Lys Lys Ile Phe Ser Ile Thr Leu Ser Leu Leu  
 1 5 10 15

Leu Ala Ser Ser Ile Leu Phe Val Ser Gly Thr Ser Thr Ala Asn Ala  
 20 25 30 A

Asn Ser Gly Phe Tyr Val Ser Gly Thr Thr Leu Tyr Asp Ala Asn Gly  
 N S 35 F Y V S 40 G T T L Y 45 D A N G

Asn Pro Phe Val Met Arg Gly Ile Asn His Gly His Ala Trp Tyr Lys  
 50 55 60

Asp Gln Ala Thr Thr Ala Ile Glu Gly Ile Ala Asn Thr Gly Ala Asn  
 65 70 75 80

Thr Val Arg Ile Val Leu Ser Asp Gly Gly Gln Trp Thr Lys Asp Asp  
 85 90 95

Ile His Thr Val Arg Asn Leu Ile Ser Leu Ala Glu Asp Asn His Leu  
 100 105 110

Val Ala Val Pro Glu Val His Asp Ala Thr Gly Tyr Asp Ser Ile Ala  
 115 120 125

Ser Leu Asn Arg Ala Val Asp Tyr Trp Ile Glu Met Arg Ser Ala Leu  
 130 135 140

209

E

Ile Gly Lys Glu Asp Thr Val Ile Ile Asn Ile Ala Asn Glu Trp Phe  
145 150 155 160

Gly Ser Trp Glu Gly Asp Ala Trp Ala Asp Gly Tyr Lys Gln Ala Ile  
165 170 175

Pro Arg Leu Arg Asn Ala Gly Leu Asn His Thr Leu Met Val Asp Ala  
180 185 190

Ala Gly Trp Gly Gln Phe Pro Gln Ser Ile His Asp Tyr Gly Arg Glu  
195 200 205

Val Phe Asn Ala Asp Pro Gln Arg Asn Thr Met Phe Ser Ile His Met  
210 215 220

Tyr Glu Tyr Ala Gly Gly Asn Ala Ser Gln Val Arg Thr Asn Ile Asp  
225 230 235 240

Arg Val Leu Asn Gln Asp Leu Ala Leu Val Ile Gly Glu Phe Gly His  
245 250 255

Arg His Thr Asn Gly Asp Val Asp Glu Ala Thr Ile Met Ser Tyr Ser  
260 265 270

Glu Gln Arg Gly Val Gly Trp Leu Ala Trp Ser Trp Lys Gly Asn Gly  
275 280 285

Pro Glu Trp Glu Tyr Leu Asp Leu Ser Asn Asp Trp Ala Gly Asn Asn  
290 295 300

Leu Thr Ala Trp Gly Asn Thr Ile Val Asn Gly Pro Tyr Gly Leu Arg  
305 310 315 320

Glu Thr Ser Arg Leu Ser Thr Val Phe Thr Gly Gly Gly Ser Asp Gly  
325 330 335

Gly Thr Ser Pro Thr Thr Leu Tyr Asp Phe Glu Gly Ser Met Gln Gly  
340 345 350

Trp Thr Gly Ser Ser Leu Ser Gly Gly Pro Trp Ala Val Thr Glu Trp  
355 360 365

3210

E

Ser Ser Lys Gly Ser His Ser Leu Lys Ala Asp Ile Gln Leu Ser Ser  
370 375 380

Asn Ser Gln His Tyr Leu His Val Ile Gln Asn Thr Ser Leu Gln Gln  
385 390 395 400

Asn Ser Arg Ile Gln Ala Thr Val Lys His Ala Asn Trp Gly Ser Val  
405 410 415

Gly Asn Gly Met Thr Ala Arg Leu Tyr Val Lys Thr Gly His Gly Tyr  
420 425 430

Thr Trp Tyr Ser Gly Ser Phe Val Pro Ile Asn Gly Ser Ser Gly Thr  
435 440 445

Thr Leu Ser Leu Asp Leu Ser Asn Val Gln Asn Leu Ser Gln Val Arg  
450 455 460

Glu Ile Gly Val Gln Phe Gln Ser Ala Ser Asp Ser Ser Gly Gln Thr  
465 470 475 480

Ser Ile Tyr Ile Asp Asn Val Ile Val Glu  
485 490

<210> 3  
<211> 1438  
<212> DNA  
<213> Bacillus sp. I633

<400> 3  
gcaaattccg gattttatgt aagcgggtacc actctatacg atgccaatgg aaaccattt 60  
gtaatgagag ggattaacca tgggcacgca tgggtataaag accaggcaac tactgcaatt 120  
gaagggattg caaataaccg tgctaatacg gtccggattg tggtatctga tgggggacaa 180  
tggacaaaag atgacatcca tacagtaaga aaccttatct ctttagcgga agataatcat 240  
ttggttgctg ttcctgaagt tcatgatgct accggttatg attccattgc ttcgctcaat 300  
cgtgctgttg attattggat tgaaatgaga agtgctttaa ttggaaagga agataccgtc 360  
attattaata ttgcgaatga atggtttggg tcgtgggaag gggatgcttg ggctgacggg 420  
tataaacaag caatcccgcg attgcgtaac gccggtctaa accatacctt gatggtagat 480  
gctgcggggg ggggacaatt tccacaatcg attcatgatt atggaagaga agtttttaat 540

gctgaccctc aacgaaatac aatgttttcg attcatatgt atgaatatgc aggtggtaat 600  
gcatcgcaag ttcgtactaa tattgaccga gttcttaatc aagacctcgc attagtcatt 660  
ggatgaatttg gacaccgtca tacaaatggg gacgtcgatg aagcaacgat tatgagctat 720  
tctgaacaaa gaggagtggg gtgggtggcg tggatcatgga aagggaaacgg cccagaatgg 780  
gagtatttag acctttcgaa tgattgggct ggaaataacc ttacagcttg gggaaatata 840  
atagtgaatg gtccatatgg ttttaagagaa acttcgagat taagcaccgt ttttacagct 900  
agcccggaac caacaccaga gccgaccgca aatacaccgg taccaggcaa tttgaagggt 960  
gaattctaca acagcaatcc ttcagatact actaactcaa tcaatcctca gttcaagggt 1020  
actaataccg gaagcagtgc aattgatttg tccaaactca cattgagata ttattataca 1080  
gtagacggac agaaagatca gaccttctgg tgtgaccatg ctgcaataat cggcagtaac 1140  
ggcagctaca acggaattac ttcaaagtga aaaggaacat ttgtaaaaat gagttcctca 1200  
acaaataacg cagacaccta ccttgaaata agctttacag gcggaactct tgaaccgggt 1260  
gcacatgttc agatacaagg tagatttgca aagaatgact ggagtaacta tacacagtca 1320  
aatgactact cattcaagtc tcgttcacag tttgttgaat gggatcaggt aacagcatac 1380  
ttgaacgggtg ttcttgtatg gggtaaagaa cccgggtggca gtgtagtata gcggccgc 1438

<210> 4  
<211> 476  
<212> PRT  
<213> Bacillus

<400> 4

Ala Asn Ser Gly Phe Tyr Val Ser Gly Thr Thr Leu Tyr Asp Ala Asn  
1 5 10 15

Gly Asn Pro Phe Val Met Arg Gly Ile Asn His Gly His Ala Trp Tyr  
20 25 30

Lys Asp Gln Ala Thr Thr Ala Ile Glu Gly Ile Ala Asn Thr Gly Ala  
35 40 45

Asn Thr Val Arg Ile Val Leu Ser Asp Gly Gly Gln Trp Thr Lys Asp  
50 55 60

Asp Ile His Thr Val Arg Asn Leu Ile Ser Leu Ala Glu Asp Asn His  
65 70 75 80

212

E

Leu Val Ala Val Pro Glu Val His Asp Ala Thr Gly Tyr Asp Ser Ile  
85 90 95

Ala Ser Leu Asn Arg Ala Val Asp Tyr Trp Ile Glu Met Arg Ser Ala  
100 105 110

Leu Ile Gly Lys Glu Asp Thr Val Ile Ile Asn Ile Ala Asn Glu Trp  
115 120 125

Phe Gly Ser Trp Glu Gly Asp Ala Trp Ala Asp Gly Tyr Lys Gln Ala  
130 135 140

Ile Pro Arg Leu Arg Asn Ala Gly Leu Asn His Thr Leu Met Val Asp  
145 150 155 160

Ala Ala Gly Trp Gly Gln Phe Pro Gln Ser Ile His Asp Tyr Gly Arg  
165 170 175

Glu Val Phe Asn Ala Asp Pro Gln Arg Asn Thr Met Phe Ser Ile His  
180 185 190

Met Tyr Glu Tyr Ala Gly Gly Asn Ala Ser Gln Val Arg Thr Asn Ile  
195 200 205

Asp Arg Val Leu Asn Gln Asp Leu Ala Leu Val Ile Gly Glu Phe Gly  
210 215 220

His Arg His Thr Asn Gly Asp Val Asp Glu Ala Thr Ile Met Ser Tyr  
225 230 235 240

Ser Glu Gln Arg Gly Val Gly Trp Leu Ala Trp Ser Trp Lys Gly Asn  
245 250 255

Gly Pro Glu Trp Glu Tyr Leu Asp Leu Ser Asn Asp Trp Ala Gly Asn  
260 265 270

Asn Leu Thr Ala Trp Gly Asn Thr Ile Val Asn Gly Pro Tyr Gly Leu  
275 280 285

Arg Glu Thr Ser Arg Leu Ser Thr Val Phe Thr Ala Ser Pro Glu Pro  
290 295 300

6 213

E

Thr Pro Glu Pro Thr Ala Asn Thr Pro Val Ser Gly Asn Leu Lys Val  
305 310 315 320

Glu Phe Tyr Asn Ser Asn Pro Ser Asp Thr Thr Asn Ser Ile Asn Pro  
325 330 335

Gln Phe Lys Val Thr Asn Thr Gly Ser Ser Ala Ile Asp Leu Ser Lys  
340 345 350

Leu Thr Leu Arg Tyr Tyr Tyr Thr Val Asp Gly Gln Lys Asp Gln Thr  
355 360 365

Phe Trp Cys Asp His Ala Ala Ile Ile Gly Ser Asn Gly Ser Tyr Asn  
370 375 380

Gly Ile Thr Ser Asn Val Lys Gly Thr Phe Val Lys Met Ser Ser Ser  
385 390 395 400

Thr Asn Asn Ala Asp Thr Tyr Leu Glu Ile Ser Phe Thr Gly Gly Thr  
405 410 415

Leu Glu Pro Gly Ala His Val Gln Ile Gln Gly Arg Phe Ala Lys Asn  
420 425 430

Asp Trp Ser Asn Tyr Thr Gln Ser Asn Asp Tyr Ser Phe Lys Ser Arg  
435 440 445

Ser Gln Phe Val Glu Trp Asp Gln Val Thr Ala Tyr Leu Asn Gly Val  
450 455 460

Leu Val Trp Gly Lys Glu Pro Gly Gly Ser Val Val  
465 470 475

<210> 5  
<211> 1482  
<212> DNA  
<213> Bacillus agaradhaerens

<400> 5  
atgaaaaaaa agttatcaca gatttatcat ttaattattt gcacacttat aataagtgtg 60  
ggaataatgg ggattacaac gtcccatca gcagcaagta caggctttta tgttgatggc 120  
aatacgttat atgacgcaaa tgggcagcca tttgtcatga gaggtattaa ccatggacat 180  
gcttggtata aagacaccgc ttcaacagct attcctgcca ttgcagagca aggcgccaac 240

214

E

acgattcgta ttgttttatc agatggcggc caatgggaaa aagacgacat tgacaccatt 300  
 cgtgaagtca ttgagcttgc ggagcaaaat aaaatgggtg ctgtcgttga agttcatgat 360  
 gccacgggtc gcgattcgcg cagtgtttaa aatcgagccg ttgattattg gatagaaatg 420  
 aaagatgcgc ttatcggtaa agaagatacg gttattatta acattgcaaa cgagtgggtat 480  
 gggagttggg atggctcagc ttgggccgat ggctatattg atgtcattcc gaagcttcgc 540  
 gatgccggct taacacacac cttaatggtt gatgcagcag gatgggggca atatccgcaa 600  
 tctattcatg attacggaca agatgtgttt aatgcagatc cgtaaaaaa tacgatgttc 660  
 tccatccata tgtatgagta tgctgggtgg gatgctaaca ctgttagatc aaatattgat 720  
 agagtcatag atcaagacct tgctctcgta ataggatgaat tcggtcatag acatactgat 780  
 ggtgatgttg atgaagatac aatccttagt tattctgaag aaactggcac aggggtggctc 840  
 gcttgggtctt ggaaaggcaa cagtaccgaa tgggactatt tagacctttc agaagactgg 900  
 gctgggtcaac atttaactga ttgggggaat agaattgtcc acggggccga tggcttacag 960  
 gaaacctcca aaccatccac cgtatttaca gatgataacg gtggtcaccc tgaaccgcca 1020  
 actgctacta ccttgatga ctttgaagga agcacacaag ggtggcatgg aagcaacgtg 1080  
 accggtggcc cttgggtccgt aacagaatgg ggtgcttcag gtaactactc tttaaaagcc 1140  
 gatgtaaatt taacctcaaa ttcttcacat gaactgtata gtgaacaaag tcgtaatcta 1200  
 cacggatact ctacagctcaa cgcaaccgtt cgccatgcca attggggaaa tcccggtaat 1260  
 ggcatgaatg caagacttta cgtgaaaacg ggctctgatt atacatggca tagcgggtcct 1320  
 ttacacgta tcaatagctc caactcagga acaacgttat cttttgattt aaacaacatc 1380  
 gaaaatagtc atcatgttag ggaaataggc gtgcaatttt cagcggcaga taatagcagt 1440  
 ggtcaaactg ctctatacgt tgataacgtt actttaagat ag 1482

<210> 6  
 <211> 493  
 <212> PRT  
 <213> Bacillus

<400> 6

Met Lys Lys Lys Leu Ser Gln Ile Tyr His Leu Ile Ile Cys Thr Leu  
 1 5 10 15

Ile Ile Ser Val Gly Ile Met Gly Ile Thr Thr Ser Pro Ser Ala Ala  
 20 25 30

8215

E



Ser Thr Gly Phe Tyr Val Asp Gly Asn Thr Leu Tyr Asp Ala Asn Gly  
35 40 45

Gln Pro Phe Val Met Arg Gly Ile Asn His Gly His Ala Trp Tyr Lys  
50 55 60

Asp Thr Ala Ser Thr Ala Ile Pro Ala Ile Ala Glu Gln Gly Ala Asn  
65 70 75 80

Thr Ile Arg Ile Val Leu Ser Asp Gly Gly Gln Trp Glu Lys Asp Asp  
85 90 95

Ile Asp Thr Ile Arg Glu Val Ile Glu Leu Ala Glu Gln Asn Lys Met  
100 105 110

Val Ala Val Val Glu Val His Asp Ala Thr Gly Arg Asp Ser Arg Ser  
115 120 125

Asp Leu Asn Arg Ala Val Asp Tyr Trp Ile Glu Met Lys Asp Ala Leu  
130 135 140

Ile Gly Lys Glu Asp Thr Val Ile Ile Asn Ile Ala Asn Glu Trp Tyr  
145 150 155 160

Gly Ser Trp Asp Gly Ser Ala Trp Ala Asp Gly Tyr Ile Asp Val Ile  
165 170 175

Pro Lys Leu Arg Asp Ala Gly Leu Thr His Thr Leu Met Val Asp Ala  
180 185 190

Ala Gly Trp Gly Gln Tyr Pro Gln Ser Ile His Asp Tyr Gly Gln Asp  
195 200 205

Val Phe Asn Ala Asp Pro Leu Lys Asn Thr Met Phe Ser Ile His Met  
210 215 220

Tyr Glu Tyr Ala Gly Gly Asp Ala Asn Thr Val Arg Ser Asn Ile Asp  
225 230 235 240

Arg Val Ile Asp Gln Asp Leu Ala Leu Val Ile Gly Glu Phe Gly His  
245 250 255

216

E

Arg His Thr Asp Gly Asp Val Asp Glu Asp Thr Ile Leu Ser Tyr Ser  
260 265 270

Glu Glu Thr Gly Thr Gly Trp Leu Ala Trp Ser Trp Lys Gly Asn Ser  
275 280 285

Thr Glu Trp Asp Tyr Leu Asp Leu Ser Glu Asp Trp Ala Gly Gln His  
290 295 300

Leu Thr Asp Trp Gly Asn Arg Ile Val His Gly Ala Asp Gly Leu Gln  
305 310 315 320

Glu Thr Ser Lys Pro Ser Thr Val Phe Thr Asp Asp Asn Gly Gly His  
325 330 335

Pro Glu Pro Pro Thr Ala Thr Thr Leu Tyr Asp Phe Glu Gly Ser Thr  
340 345 350

Gln Gly Trp His Gly Ser Asn Val Thr Gly Gly Pro Trp Ser Val Thr  
355 360 365

Glu Trp Gly Ala Ser Gly Asn Tyr Ser Leu Lys Ala Asp Val Asn Leu  
370 375 380

Thr Ser Asn Ser Ser His Glu Leu Tyr Ser Glu Gln Ser Arg Asn Leu  
385 390 395 400

His Gly Tyr Ser Gln Leu Asn Ala Thr Val Arg His Ala Asn Trp Gly  
405 410 415

Asn Pro Gly Asn Gly Met Asn Ala Arg Leu Tyr Val Lys Thr Gly Ser  
420 425 430

Asp Tyr Thr Trp His Ser Gly Pro Phe Thr Arg Ile Asn Ser Ser Asn  
435 440 445

Ser Gly Thr Thr Leu Ser Phe Asp Leu Asn Asn Ile Glu Asn Ser His  
450 455 460

His Val Arg Glu Ile Gly Val Gln Phe Ser Ala Ala Asp Asn Ser Ser  
465 470 475 480

Gly Gln Thr Ala Leu Tyr Val Asp Asn Val Thr Leu Arg  
485 490

<210> 7  
<211> 1407  
<212> DNA  
<213> *Bacillus agaradhaerens*

<400> 7  
atgaaaaaaa agttatcaca gatttatcat ttaattatTT gcacacttat aataagtgtg 60  
ggaataatgg ggattacaac gtcccatca gcagcaagta caggctttta tgttgatggc 120  
aatacgttat atgacgcaaa tgggcagcca tttgtcatga gaggtattaa ccatggacat 180  
gcttggtata aagacaccgc ttcaacagct attcctgcca ttgcagagca aggcgccaac 240  
acgattcgta ttgttttatc agatggcggg caatgggaaa aagacgacat tgacaccatt 300  
cgtgaagtca ttgagcttgc ggagcaaaat aaaatgggtg ctgtcgttga agttcatgat 360  
gccacgggtc gcgattcgcg cagtgattta aatcgagccg ttgattattg gatagaaatg 420  
aaagatgcgc ttatcggtaa agaagatacg gttattatta acattgcaaa cgagtgggat 480  
gggagttggg atggctcagc ttgggccgat ggctatattg atgtcattcc gaagcttcgc 540  
gatgccggct taacacacac cttaatggtt gatgcagcag gatgggggca atatccgcaa 600  
tctattcatg attacggaca agatgtgttt aatgcagatc cgtaaaaaaa tacgatgttc 660  
tccatccata tgtatgagta tgctggtggt gatgctaaca ctgttagatc aaatattgat 720  
agagtcatag atcaagacct tgctctcgta ataggtgaat tcggtcatag acatactgat 780  
ggtgatgttg atgaagatac aatccttagt tattctgaag aaactggcac aggggtggctc 840  
gcttggtctt ggaaaaggcaa cagtaccgaa tgggactatt tagacctttc agaagactgg 900  
gctggtcaac atttaactga ttgggggaat agaattgtcc acggggccga tggcttacag 960  
gaaacctcca aaccatccac cgtattttaca gatgataacg gtggtcaccc tgaaccgcca 1020  
actgctacta ccttgatatga ctttgaagga agcacacaag ggtggcatgg aagcaacgtg 1080  
accggtggcc cttggtccgt aacagaatgg ggtgcttcag gtaactactc tttaaaaagcc 1140  
gatgtaaaatt taacctcaaa ttcttcacat gaactgtata gtgaacaaaag tcgtaatcta 1200  
cacggatact ctcagctcaa cgcaaccgtt cgccatgcca attggggaaa tcccggtaat 1260  
ggcatgaatg caagacttta cgtgaaaacg ggctctgatt atacatggca tagcggtcct 1320  
tttacacgta tcaatagctc caactcagga acaacgttat cttttgattt aaacaacatc 1380  
gaaaatatca tcatgttagg gaaatag 1407

<210> 8  
<211> 468  
<212> PRT  
<213> Bacillus agaradhaerens

<400> 8

Met Lys Lys Lys Leu Ser Gln Ile Tyr His Leu Ile Ile Cys Thr Leu  
1 5 10 15

Ile Ile Ser Val Gly Ile Met Gly Ile Thr Thr Ser Pro Ser Ala Ala  
20 25 30

Ser Thr Gly Phe Tyr Val Asp Gly Asn Thr Leu Tyr Asp Ala Asn Gly  
35 40 45

Gln Pro Phe Val Met Arg Gly Ile Asn His Gly His Ala Trp Tyr Lys  
50 55 60

Asp Thr Ala Ser Thr Ala Ile Pro Ala Ile Ala Glu Gln Gly Ala Asn  
65 70 75 80

Thr Ile Arg Ile Val Leu Ser Asp Gly Gly Gln Trp Glu Lys Asp Asp  
85 90 95

Ile Asp Thr Ile Arg Glu Val Ile Glu Leu Ala Glu Gln Asn Lys Met  
100 105 110

Val Ala Val Val Glu Val His Asp Ala Thr Gly Arg Asp Ser Arg Ser  
115 120 125

Asp Leu Asn Arg Ala Val Asp Tyr Trp Ile Glu Met Lys Asp Ala Leu  
130 135 140

Ile Gly Lys Glu Asp Thr Val Ile Ile Asn Ile Ala Asn Glu Trp Tyr  
145 150 155 160

Gly Ser Trp Asp Gly Ser Ala Trp Ala Asp Gly Tyr Ile Asp Val Ile  
165 170 175

Pro Lys Leu Arg Asp Ala Gly Leu Thr His Thr Leu Met Val Asp Ala  
180 185 190

Ala Gly Trp Gly Gln Tyr Pro Gln Ser Ile His Asp Tyr Gly Gln Asp  
195 200 205

Val Phe Asn Ala Asp Pro Leu Lys Asn Thr Met Phe Ser Ile His Met  
210 215 220

Tyr Glu Tyr Ala Gly Gly Asp Ala Asn Thr Val Arg Ser Asn Ile Asp  
225 230 235 240

Arg Val Ile Asp Gln Asp Leu Ala Leu Val Ile Gly Glu Phe Gly His  
245 250 255

Arg His Thr Asp Gly Asp Val Asp Glu Asp Thr Ile Leu Ser Tyr Ser  
260 265 270

Glu Glu Thr Gly Thr Gly Trp Leu Ala Trp Ser Trp Lys Gly Asn Ser  
275 280 285

Thr Glu Trp Asp Tyr Leu Asp Leu Ser Glu Asp Trp Ala Gly Gln His  
290 295 300

Leu Thr Asp Trp Gly Asn Arg Ile Val His Gly Ala Asp Gly Leu Gln  
305 310 315 320

Glu Thr Ser Lys Pro Ser Thr Val Phe Thr Asp Asp Asn Gly Gly His  
325 330 335

Pro Glu Pro Pro Thr Ala Thr Thr Leu Tyr Asp Phe Glu Gly Ser Thr  
340 345 350

Gln Gly Trp His Gly Ser Asn Val Thr Gly Gly Pro Trp Ser Val Thr  
355 360 365

Glu Trp Gly Ala Ser Gly Asn Tyr Ser Leu Lys Ala Asp Val Asn Leu  
370 375 380

Thr Ser Asn Ser Ser His Glu Leu Tyr Ser Glu Gln Ser Arg Asn Leu  
385 390 395 400

His Gly Tyr Ser Gln Leu Asn Ala Thr Val Arg His Ala Asn Trp Gly  
405 410 415

Asn Pro Gly Asn Gly Met Asn Ala Arg Leu Tyr Val Lys Thr Gly Ser

420

425

430

Asp Tyr Thr Trp His Ser Gly Pro Phe Thr Arg Ile Asn Ser Ser Asn  
 435 440 445

Ser Gly Thr Thr Leu Ser Phe Asp Leu Asn Asn Ile Glu Asn Ile Ile  
 450 455 460

Met Leu Gly Lys  
 465

<210> 9  
 <211> 1761  
 <212> DNA  
 <213> Bacillus halodurans

<400> 9  
 atgaaaagta taaagaaatt ggtagtcgtt tgcattggcat ttctattaat ttttccatcg 60  
 acgtcatttg ctttttctgg aagcgtttca gcttcagggtc aagagcttaa aatgacagat 120  
 caaaacgcat ctcaatatac aaaagagttg tttgcctttt tacgtgatgt aagtggtaaa 180  
 caagttttat ttggtcaaca acacgcaact gatgagggat taacacttag aggaacaggt 240  
 aaccgaattg gttcaacaga atcagaagtg aaaaatgctg ttggtgatta tcttgctggt 300  
 tttggttggg atacaaacag tctagatggt agagaaaagc ccgtaaatga tgaaccgagt 360  
 caagaacaaa gaatcttaaa tacagcagct tcaatgaagg cagctcacga cttaggtggg 420  
 attatcacac taagtatgca tcctgataac tttgtaacag gaggggctta tggcgataca 480  
 actggaaaatg ttgtacaaga aattcttcct ggtggatcaa agcatgaaga attcaatgca 540  
 tggttggata acctagcggc tttagctcac gaattaaagg atgacaacgg gaaacacatt 600  
 ccaattatth tccgtccttt ccatgagcaa acaggttctt ggttctggtg gggagcaagc 660  
 acaacaactc cagaacagta taaagctatt tacagatata cggttgaata cttacgtgac 720  
 gtaaaaggag caaacaactt cttatacgtt ttttctcctg gtgcagggtc agctggcgat 780  
 ttaaactcgtt atatggaaac ttaccctggt gatgattatg tcgatatctt tggattgat 840  
 aactatgaca ataaatcaaa tgctggatca gaagcttga tacaaggtgt tgtaaccgat 900  
 ttagctatgc ttgttgattt agctgaagaa aaaggaaaga ttgctgcgtt taccgagtat 960  
 ggttacagtg caacaggtat gaatcgtact ggtaacacat tggattggta tactcgttta 1020  
 cttaatgcaa taaaagaaga tccaaaagca agtaagattt cttacatgct tacatgggca 1080

aactttggtt tccctaacaa tatgtatggt ccttacaaag acattcacgg tgatttaggt 1140  
ggagatcatg aactccttcc agatttcacg aaattttttg aagatgatta ctcagctttc 1200  
acaggagata tcaagggaaa tgtgtatgat acaggaattg aatatactgt agcaccacat 1260  
gaacgtttta tgtatgtgct ttcgcctatt actggaacaa cgataacaga tactgttaca 1320  
ttacgagcta aagtattaaa cgatgataac gcagttgtta cgtacagggt tgaagggttct 1380  
gacgttgaac atgaaatgac gttagctgac tcgggatact acacagctaa gtattctccg 1440  
acggcagaag taaatggtgg atcagttgat ttaacagtta cgtactgggtc tggagaagaa 1500  
aaagtacaag atgaagtgat tagactttat gtaaaggctt cagaaatctc actttacaag 1560  
cttacgtttg atgaggatat taatggaatt aagtcgaatg gcacttggcc tgaagatggt 1620  
attacatctg acgttttctca tgtcagtttt gacggaaatg ggaaattgaa gtttgcagtt 1680  
aatggaatgt catccgaaga gtggtggcaa gaacttaa atagaattaac agatctttct 1740  
gatgtgaatt tagccaagta a 1761

<210> 10  
<211> 586  
<212> PRT  
<213> Bacillus halodurans

<400> 10

Met Lys Ser Ile Lys Lys Leu Val Val Val Cys Met Ala Phe Leu Leu  
1 5 10 15

Ile Phe Pro Ser Thr Ser Phe Ala Phe Ser Gly Ser Val Ser Ala Ser  
20 25 30

Gly Gln Glu Leu Lys Met Thr Asp Gln Asn Ala Ser Gln Tyr Thr Lys  
35 40 45

Glu Leu Phe Ala Phe Leu Arg Asp Val Ser Gly Lys Gln Val Leu Phe  
50 55 60

Gly Gln Gln His Ala Thr Asp Glu Gly Leu Thr Leu Arg Gly Thr Gly  
65 70 75 80

Asn Arg Ile Gly Ser Thr Glu Ser Glu Val Lys Asn Ala Val Gly Asp  
85 90 95

Tyr Pro Ala Val Phe Gly Trp Asp Thr Asn Ser Leu Asp Gly Arg Glu

100

105

110

Lys Pro Gly Asn Asp Glu Pro Ser Gln Glu Gln Arg Ile Leu Asn Thr  
115 120 125

Ala Ala Ser Met Lys Ala Ala His Asp Leu Gly Gly Ile Ile Thr Leu  
130 135 140

Ser Met His Pro Asp Asn Phe Val Thr Gly Gly Ala Tyr Gly Asp Thr  
145 150 155 160

Thr Gly Asn Val Val Gln Glu Ile Leu Pro Gly Gly Ser Lys His Glu  
165 170 175

Glu Phe Asn Ala Trp Leu Asp Asn Leu Ala Ala Leu Ala His Glu Leu  
180 185 190

Lys Asp Asp Asn Gly Lys His Ile Pro Ile Ile Phe Arg Pro Phe His  
195 200 205

Glu Gln Thr Gly Ser Trp Phe Trp Trp Gly Ala Ser Thr Thr Thr Pro  
210 215 220

Glu Gln Tyr Lys Ala Ile Tyr Arg Tyr Thr Val Glu Tyr Leu Arg Asp  
225 230 235 240

Val Lys Gly Ala Asn Asn Phe Leu Tyr Gly Phe Ser Pro Gly Ala Gly  
245 250 255

Pro Ala Gly Asp Leu Asn Arg Tyr Met Glu Thr Tyr Pro Gly Asp Asp  
260 265 270

Tyr Val Asp Ile Phe Gly Ile Asp Asn Tyr Asp Asn Lys Ser Asn Ala  
275 280 285

Gly Ser Glu Ala Trp Ile Gln Gly Val Val Thr Asp Leu Ala Met Leu  
290 295 300

Val Asp Leu Ala Glu Glu Lys Gly Lys Ile Ala Ala Phe Thr Glu Tyr  
305 310 315 320

Gly Tyr Ser Ala Thr Gly Met Asn Arg Thr Gly Asn Thr Leu Asp Trp  
325 330 335



Tyr Thr Arg Leu Leu Asn Ala Ile Lys Glu Asp Pro Lys Ala Ser Lys  
340 345 350

Ile Ser Tyr Met Leu Thr Trp Ala Asn Phe Gly Phe Pro Asn Asn Met  
355 360 365

Tyr Val Pro Tyr Lys Asp Ile His Gly Asp Leu Gly Gly Asp His Glu  
370 375 380

Leu Leu Pro Asp Phe Ile Lys Phe Phe Glu Asp Asp Tyr Ser Ala Phe  
385 390 395 400

Thr Gly Asp Ile Lys Gly Asn Val Tyr Asp Thr Gly Ile Glu Tyr Thr  
405 410 415

Val Ala Pro His Glu Arg Leu Met Tyr Val Leu Ser Pro Ile Thr Gly  
420 425 430

Thr Thr Ile Thr Asp Thr Val Thr Leu Arg Ala Lys Val Leu Asn Asp  
435 440 445

Asp Asn Ala Val Val Thr Tyr Arg Val Glu Gly Ser Asp Val Glu His  
450 455 460

Glu Met Thr Leu Ala Asp Ser Gly Tyr Tyr Thr Ala Lys Tyr Ser Pro  
465 470 475 480

Thr Ala Glu Val Asn Gly Gly Ser Val Asp Leu Thr Val Thr Tyr Trp  
485 490 495

Ser Gly Glu Glu Lys Val Gln Asp Glu Val Ile Arg Leu Tyr Val Lys  
500 505 510

Ala Ser Glu Ile Ser Leu Tyr Lys Leu Thr Phe Asp Glu Asp Ile Asn  
515 520 525

Gly Ile Lys Ser Asn Gly Thr Trp Pro Glu Asp Gly Ile Thr Ser Asp  
530 535 540

Val Ser His Val Ser Phe Asp Gly Asn Gly Lys Leu Lys Phe Ala Val  
545 550 555 560

Asn Gly Met Ser Ser Glu Glu Trp Trp Gln Glu Leu Lys Leu Glu Leu  
 565 570 575

Thr Asp Leu Ser Asp Val Asn Leu Ala Lys  
 580 585

<210> 11  
 <211> 995  
 <212> DNA  
 <213> Bacillus sp. AAI12

E  
 <400> 11  
 gtgtataagc ttaccatac gtattttggt gcgttaattt gttctatttt gatctttgct 60  
 ggggttttaa atacttcttc ttcacaagca gaagcccatc acagtgggtt ccatgttaat 120  
 ggtacaacat tatatgatgc aaatggaaac ccttttggtt tgagagggat taatcatgga 180  
 catgcttggt ttaaacaaga actagaaaca tccatgagag ggattagtca aacaggggca 240  
 aatacgattc gtgtcgtttt gtctaattggg caaagatggc aaaaagatga tcgaaacatg 300  
 gtagcttcgg ttatttcttt ggcagagcag catcaaatga ttgccgtttt agaagttcat 360  
 gatgctactg gtagcaataa tttctccgat ctgcaagctg ctgtggacta ttggattgag 420  
 atgaaggatg ttttgcaggg gaaagaggac atagtgatca ttaatatcgc caatgaatgg 480  
 tacggtgctt gggacggagg cgcattgggca cgaggggtatc agaatgcgat acgtcagctt 540  
 cgaaatgcag gcttgtcaca tacatttatg gttgacgctg ccggttatgg ccagtaccct 600  
 caatcggtag ttgattatgg tcaagaagta ttaaatgctg acccacagag aaacacaatg 660  
 ttttctgttc atatgtatga atatgcaggc ggagatgcta atacagtaag acgaaacatt 720  
 gactcgatct taagccagaa cttagctctt gtcattgggtg aattcgggca ttggcattat 780  
 gacggtgatg ttgatgagga caccatttta agctattcac agcaaagaaa tgtgggatgg 840  
 ttggcgtgga gctggcatgg caatagtga ggggtcgaat atcttgattt atcgaatgac 900  
 tttgctggta atcgactgac atgggtgggt gatcgaatag taaacgggtcc gaatgggatt 960  
 cgtcaaacct ctaaaagaag cagtgtgttt caata 995

<210> 12  
 <211> 331  
 <212> PRT  
 <213> Bacillus sp. AAI12

<400> 12

Val Tyr Lys Leu Thr His Thr Tyr Phe Val Ala Leu Ile Cys Ser Ile  
1 5 10 15

Leu Ile Phe Ala Gly Val Leu Asn Thr Ser Ser Ser Gln Ala Glu Ala  
20 25 30

His His Ser Gly Phe His Val Asn Gly Thr Thr Leu Tyr Asp Ala Asn  
35 40 45

Gly Asn Pro Phe Val Met Arg Gly Ile Asn His Gly His Ala Trp Phe  
50 55 60

Lys Gln Glu Leu Glu Thr Ser Met Arg Gly Ile Ser Gln Thr Gly Ala  
65 70 75 80

Asn Thr Ile Arg Val Val Leu Ser Asn Gly Gln Arg Trp Gln Lys Asp  
85 90 95

Asp Arg Asn Met Val Ala Ser Val Ile Ser Leu Ala Glu Gln His Gln  
100 105 110

Met Ile Ala Val Leu Glu Val His Asp Ala Thr Gly Ser Asn Asn Phe  
115 120 125

Ser Asp Leu Gln Ala Ala Val Asp Tyr Trp Ile Glu Met Lys Asp Val  
130 135 140

Leu Gln Gly Lys Glu Asp Ile Val Ile Ile Asn Ile Ala Asn Glu Trp  
145 150 155 160

Tyr Gly Ala Trp Asp Gly Gly Ala Trp Ala Arg Gly Tyr Gln Asn Ala  
165 170 175

Ile Arg Gln Leu Arg Asn Ala Gly Leu Ser His Thr Phe Met Val Asp  
180 185 190

Ala Ala Gly Tyr Gly Gln Tyr Pro Gln Ser Val Val Asp Tyr Gly Gln  
195 200 205

Glu Val Leu Asn Ala Asp Pro Gln Arg Asn Thr Met Phe Ser Val His  
210 215 220

Met Tyr Glu Tyr Ala Gly Gly Asp Ala Asn Thr Val Arg Arg Asn Ile

225

230

235

240

Asp Ser Ile Leu Ser Gln Asn Leu Ala Leu Val Ile Gly Glu Phe Gly  
245 250 255

His Trp His Tyr Asp Gly Asp Val Asp Glu Asp Thr Ile Leu Ser Tyr  
260 265 270

Ser Gln Gln Arg Asn Val Gly Trp Leu Ala Trp Ser Trp His Gly Asn  
275 280 285

Ser Glu Gly Val Glu Tyr Leu Asp Leu Ser Asn Asp Phe Ala Gly Asn  
290 295 300

Arg Leu Thr Trp Trp Gly Asp Arg Ile Val Asn Gly Pro Asn Gly Ile  
305 310 315 320

Arg Gln Thr Ser Lys Arg Ser Ser Val Phe Gln  
325 330

<210> 13

<211> 1464

<212> DNA

<213> Humicola insolens

<400> 13

atggcaaaagg ctctgaagta ctttgcctgg ggccttgctg ccctggcctc gggcgctgtt 60  
gccgctcctt actgtgctcc ccagccgtcg acaacctctc aggagcctac gagcactccg 120  
tcgcctgtgc ccggtccgcg gaccttcgaa gcggaggatg ccatcctcac gggcacgagg 180  
gttgagtcga gcctcgccgg ctactctggt accggatatg tagcgggctt cgacgagccc 240  
agtgacaaga tcacgttcca cgtggacagc gagaccacac ggctgtacga cctcaccatc 300  
cgcggtggccg ccatctatgg cgagaagcgc accaccgtcg tgctcaataa cggcgcgggca 360  
agtgaggctc acttcccggc aggcgattcg ttcgtcgaca tcgctgccgg ccaggtcctg 420  
ctgaaccagg gcgacaacac catcgacatt gtcaacaact ggggatggta cctgatcgac 480  
tccatcacca tcaccccctc cgccccgcga cccctcacc aaatcaaccc ttcccccgtc 540  
aaccctgccg ccgacgacaa cgcgcgggcg ttgtacgcat acctccgctc catctacggc 600  
aagaaaatcc tttccggcca gcaggagctt tcctggggcga actggatcgc ccaacagacg 660  
ggcaaaaactc ccgcgctggt gtccgtcgat atgatggatt attcccctag tcgggtggaa 720

agaggcactg tcgggtctgc cgtcgaggag gccatcgagc atcaccggcg cggcggcatt 780  
 gtctcggtgt tgtggcactg gaacgcgccc acggggctgt acgacacgcc cgagcgccgg 840  
 tgggtggagcg ggttctacac ggacgcgacc gactttgacg tcgcgcgggc gctggcggat 900  
 acgacgaatg ccaactacac gctgctgacg cgggatatcg acgcgatcgc ggtgcagctc 960  
 aagaggttgc gggacgcggg cgtgccggtg ctttggcgcc cgctgcacga ggccgagggc 1020  
 ggttggtttt ggtggggagc gaagggcccg gaggcataca agaagctgtg ggggattctg 1080  
 tatgaccgac tcacgaacta ccatgggctg aataacctgc tgtgggtgtg gaactcgatc 1140  
 ctacccgagt ggtatcccgg agacgaaaca gtagacattg tcagcgcgga cgtgtacgcg 1200  
 cagggtaatg ggcccattgc gacgcagtat aaccagctca tcgagctggg caaggacaag 1260  
 aagatgatcg cggcgactga ggtcggggcc gcgccgctgc cggacctgtt gcaggcctat 1320  
 gaggctcact ggttgtggtt cgctgttttg ggagacacgt tcatcaacaa ccctcagtgg 1380  
 aactcgatcg agaccttgaa gacgatctac aatagcgact atgttctcac tctcgatgag 1440  
 attcaggggt ggaggaacgc gcaa 1464

<210> 14  
 <211> 488  
 <212> PRT  
 <213> Humicola insolens

<400> 14

Met Ala Lys Ala Leu Lys Tyr Phe Ala Trp Gly Leu Ala Ala Leu Ala  
 1 5 10 15

Ser Gly Ala Val Ala Ala Pro Tyr Cys Ala Pro Gln Pro Ser Thr Thr  
 20 25 30

Ser Gln Glu Pro Thr Ser Thr Pro Ser Pro Val Pro Gly Pro Arg Thr  
 35 40 45

Phe Glu Ala Glu Asp Ala Ile Leu Thr Gly Thr Arg Val Glu Ser Ser  
 50 55 60

Leu Ala Gly Tyr Ser Gly Thr Gly Tyr Val Ala Gly Phe Asp Glu Pro  
 65 70 75 80

Ser Asp Lys Ile Thr Phe His Val Asp Ser Glu Thr Thr Arg Leu Tyr  
 85 90 95

228

E

Asp Leu Thr Ile Arg Val Ala Ala Ile Tyr Gly Glu Lys Arg Thr Thr  
100 105 110

Val Val Leu Asn Asn Gly Ala Ala Ser Glu Val Tyr Phe Pro Ala Gly  
115 120 125

Asp Ser Phe Val Asp Ile Ala Ala Gly Gln Val Leu Leu Asn Gln Gly  
130 135 140

E Asp Asn Thr Ile Asp Ile Val Asn Asn Trp Gly Trp Tyr Leu Ile Asp  
145 150 155 160

Ser Ile Thr Ile Thr Pro Ser Ala Pro Arg Pro Pro His Gln Ile Asn  
165 170 175

Pro Ser Pro Val Asn Pro Ala Ala Asp Asp Asn Ala Arg Ala Leu Tyr  
180 185 190

Ala Tyr Leu Arg Ser Ile Tyr Gly Lys Lys Ile Leu Ser Gly Gln Gln  
195 200 205

Glu Leu Ser Trp Ala Asn Trp Ile Ala Gln Gln Thr Gly Lys Thr Pro  
210 215 220

Ala Leu Val Ser Val Asp Met Met Asp Tyr Ser Pro Ser Arg Val Glu  
225 230 235 240

Arg Gly Thr Val Gly Ser Ala Val Glu Glu Ala Ile Glu His His Arg  
245 250 255

Arg Gly Gly Ile Val Ser Val Leu Trp His Trp Asn Ala Pro Thr Gly  
260 265 270

Leu Tyr Asp Thr Pro Glu Arg Arg Trp Trp Ser Gly Phe Tyr Thr Asp  
275 280 285

Ala Thr Asp Phe Asp Val Ala Arg Ala Leu Ala Asp Thr Thr Asn Ala  
290 295 300

Asn Tyr Thr Leu Leu Ile Arg Asp Ile Asp Ala Ile Ala Val Gln Leu  
305 310 315 320

Lys Arg Leu Arg Asp Ala Gly Val Pro Val Leu Trp Arg Pro Leu His  
 325 330 335

Glu Ala Glu Gly Gly Trp Phe Trp Trp Gly Ala Lys Gly Pro Glu Ala  
 340 345 350

Tyr Lys Lys Leu Trp Gly Ile Leu Tyr Asp Arg Leu Thr Asn Tyr His  
 355 360 365

Gly Leu Asn Asn Leu Leu Trp Val Trp Asn Ser Ile Leu Pro Glu Trp  
 370 375 380

Tyr Pro Gly Asp Glu Thr Val Asp Ile Val Ser Ala Asp Val Tyr Ala  
 385 390 395 400

Gln Gly Asn Gly Pro Met Ser Thr Gln Tyr Asn Gln Leu Ile Glu Leu  
 405 410 415

Gly Lys Asp Lys Lys Met Ile Ala Ala Thr Glu Val Gly Ala Ala Pro  
 420 425 430

Leu Pro Asp Leu Leu Gln Ala Tyr Glu Ala His Trp Leu Trp Phe Ala  
 435 440 445

Val Trp Gly Asp Thr Phe Ile Asn Asn Pro Gln Trp Asn Ser Ile Glu  
 450 455 460

Thr Leu Lys Thr Ile Tyr Asn Ser Asp Tyr Val Leu Thr Leu Asp Glu  
 465 470 475 480

Ile Gln Gly Trp Arg Asn Ala Gln  
 485

<210> 15  
 <211> 1107  
 <212> DNA  
 <213> Bacillus sp. AA349

<400> 15  
 atgagaagta tgaagctttt atttgctatg tttatttttag ttttttcctc ttttactttt 60  
 aacttagtag ttgcgcaagc tagtggacat gggcaaagtc ataaagtacc ttgggcacca 120  
 caagctgaag cacctggaaa aacggctgaa aatggagtct gggataaagt tcgaaataat 180  
 cctggaaaag ccaatcctcc agcaggaaaa gtcaatgggt tttatataga tggaacaacc 240

230

E

ttatatgatg caaatggtaa gccatttgtg atgcgtggaa ttaaccacgg tcattcatgg 300  
 tacaagcctc acatagaaac cgcgatggag gcaattgctg atactggagc aaactccatt 360  
 cgtgtagtgc tctcagatgg acaacagtgg accaaagatg atgttgacga agtagcaaaa 420  
 attatatctt tagcagaaaa acattcttta gttgctgctc ttgaggtaca tgatgcactc 480  
 ggaacagatg atattgaacc attacttaaa acagttgatt actggattga gatcaaagat 540  
 gctttaatcg gaaaagagga caaagtaatt attaacattt ctaatgaatg gtttggttct 600  
 tggagcagtg aaggttgggc agatggatat aaaaaagcaa ttcctttact aagagaggcg 660  
 ggtctaaaac atacacttat ggttgacgca gctgggtggg gacaatttcc tagatctatt 720  
 catgaaaaag gattagaagt ttttaactca gacccattaa agaatacaat gttttccatt 780  
 catatgtatg aatgggcagc gggtaatcct caacaagtaa aagacaatat tgacgggtgtt 840  
 cttgaaaaga atttagctgt agtaattggg gagttcggtc atcatcacta cggaagagat 900  
 gttgctgttg atacaatctt aagtcattct gagaagtatg atgtagggtg gcttgcttgg 960  
 tcttggcacg gaaatagtgg tgggtgtagag tatcttgact tagcaacaga tttctcaggg 1020  
 acacaactaa ctgaatgggg agaaagaatt gtacacgggc cgaatgggtt aaaagaaaact 1080  
 tctgaaatcg ttagtgtata caaaaaa 1107

<210> 16  
 <211> 369  
 <212> PRT  
 <213> Bacillus sp.

<400> 16

Met Arg Ser Met Lys Leu Leu Phe Ala Met Phe Ile Leu Val Phe Ser  
 1 5 10 15

Ser Phe Thr Phe Asn Leu Val Val Ala Gln Ala Ser Gly His Gly Gln  
 20 25 30

Met His Lys Val Pro Trp Ala Pro Gln Ala Glu Ala Pro Gly Lys Thr  
 35 40 45

Ala Glu Asn Gly Val Trp Asp Lys Val Arg Asn Asn Pro Gly Lys Ala  
 50 55 60

Asn Pro Pro Ala Gly Lys Val Asn Gly Phe Tyr Ile Asp Gly Thr Thr  
 65 70 75 80



Leu Tyr Asp Ala Asn Gly Lys Pro Phe Val Met Arg Gly Ile Asn His  
85 90 95

Gly His Ser Trp Tyr Lys Pro His Ile Glu Thr Ala Met Glu Ala Ile  
100 105 110

Ala Asp Thr Gly Ala Asn Ser Ile Arg Val Val Leu Ser Asp Gly Gln  
115 120 125

Gln Trp Thr Lys Asp Asp Val Asp Glu Val Ala Lys Ile Ile Ser Leu  
130 135 140

Ala Glu Lys His Ser Leu Val Ala Ala Leu Glu Val His Asp Ala Leu  
145 150 155 160

Gly Thr Asp Asp Ile Glu Pro Leu Leu Lys Thr Val Asp Tyr Trp Ile  
165 170 175

Glu Ile Lys Asp Ala Leu Ile Gly Lys Glu Asp Lys Val Ile Ile Asn  
180 185 190

Ile Ser Asn Glu Trp Phe Gly Ser Trp Ser Ser Glu Gly Trp Ala Asp  
195 200 205

Gly Tyr Lys Lys Ala Ile Pro Leu Leu Arg Glu Ala Gly Leu Lys His  
210 215 220

Thr Leu Met Val Asp Ala Ala Gly Trp Gly Gln Phe Pro Arg Ser Ile  
225 230 235 240

His Glu Lys Gly Leu Glu Val Phe Asn Ser Asp Pro Leu Lys Asn Thr  
245 250 255

Met Phe Ser Ile His Met Tyr Glu Trp Ala Ala Gly Asn Pro Gln Gln  
260 265 270

Val Lys Asp Asn Ile Asp Gly Val Leu Glu Lys Asn Leu Ala Val Val  
275 280 285

Ile Gly Glu Phe Gly His His His Tyr Gly Arg Asp Val Ala Val Asp  
290 295 300

Thr Ile Leu Ser His Ser Glu Lys Tyr Asp Val Gly Trp Leu Ala Trp  
305 310 315 320

Ser Trp His Gly Asn Ser Gly Gly Val Glu Tyr Leu Asp Leu Ala Thr  
325 330 335

Asp Phe Ser Gly Thr Gln Leu Thr Glu Trp Gly Glu Arg Ile Val His  
340 345 350

Gly Pro Asn Gly Leu Lys Glu Thr Ser Glu Ile Val Ser Val Tyr Lys  
355 360 365

Lys

<210> 17  
<211> 915  
<212> DNA  
<213> Bacillus sp.

<400> 17  
atctcaacac tcagaaatgc cggatttcgc aatacaatcg ttgtggatgc atcgggggtgg 60  
ggacaaaatt catcgccaat taaagcttat ggcaacgaag tgtaaacca tgatccgcag 120  
cgcaatgtta tggttctccat acacatgtac ggttcctgga ataatcagtc gcgaatcggc 180  
agcgaattgc aggccatcaa agaccttggc cttgctgtca tgattgggtga attcggatac 240  
aactacaaca acggcaataa caacttgggg agtcagggtta acgcccagga aatcatgaat 300  
caggcgcaag caaaaaggaat cggctacatg ccgtggctcg ggactggcaa tgacgcggct 360  
aactcttggc ttgatattgac aacaaacgat tggcaaacac ttacatcatg ggggaatcta 420  
gttgtaaatg gaaccaacgc cattcgagct acgtctgtcc cagcaactgt atttaataca 480  
caaacaacaa tttatgattt tgaaggcggc aatgcccagg gctggtcagg ttccggtttg 540  
agcggggggc cttggtctgt taatgaatgg gcggcgagcg gtagttattc tctcaaagcg 600  
aatatatctc taggcgccac tcaaaaagct ttgcaaacca cagcgtccca taatttcagc 660  
ggccggtcta cattatccgt aagagtaaag catgcagcat ggggaaatca cggcagcggc 720  
atgcaagcca agttatatgt gaaaacaggg gccggttacg cctgggtatga tggcggcact 780  
gtaaacatca acagctcggg caacacattg acgctaaacc tggcaggcat tcctaattctg 840  
aacgacgtca gagaactcgg aattgaattt ataacacctg caaattcgag tggttctttc 900

gcaatttatg ttgac

915

<210> 18  
<211> 305  
<212> PRT  
<213> Bacillus sp.

<400> 18

Ile Ser Thr Leu Arg Asn Ala Gly Ile Arg Asn Thr Ile Val Val Asp  
1 5 10 15

Ala Ser Gly Trp Gly Gln Asn Ser Ser Pro Ile Lys Ala Tyr Gly Asn  
20 25 30

Glu Val Leu Asn His Asp Pro Gln Arg Asn Val Met Phe Ser Ile His  
35 40 45

Met Tyr Gly Ser Trp Asn Asn Gln Ser Arg Ile Gly Ser Glu Leu Gln  
50 55 60

Ala Ile Lys Asp Leu Gly Leu Ala Val Met Ile Gly Glu Phe Gly Tyr  
65 70 75 80

Asn Tyr Asn Asn Gly Asn Asn Asn Leu Gly Ser Gln Val Asn Ala Gln  
85 90 95

Glu Ile Met Asn Gln Ala Gln Ala Lys Gly Ile Gly Tyr Met Pro Trp  
100 105 110

Ser Trp Thr Gly Asn Asp Ala Ala Asn Ser Trp Leu Asp Met Thr Thr  
115 120 125

Asn Asp Trp Gln Thr Leu Thr Ser Trp Gly Asn Leu Val Val Asn Gly  
130 135 140

Thr Asn Gly Ile Arg Ala Thr Ser Val Pro Ala Thr Val Phe Asn Thr  
145 150 155 160

Gln Thr Thr Ile Tyr Asp Phe Glu Gly Gly Asn Ala Gln Gly Trp Ser  
165 170 175

Gly Ser Gly Leu Ser Gly Gly Pro Trp Ser Val Asn Glu Trp Ala Ala  
180 185 190

Ser Gly Ser Tyr Ser Leu Lys Ala Asn Ile Ser Leu Gly Ala Thr Gln  
195 200 205

Lys Ala Leu Gln Thr Thr Ala Ser His Asn Phe Ser Gly Arg Ser Thr  
210 215 220

Leu Ser Val Arg Val Lys His Ala Ala Trp Gly Asn His Gly Ser Gly  
225 230 235 240

Met Gln Ala Lys Leu Tyr Val Lys Thr Gly Ala Gly Tyr Ala Trp Tyr  
245 250 255

Asp Gly Gly Thr Val Asn Ile Asn Ser Ser Gly Asn Thr Leu Thr Leu  
260 265 270

Asn Leu Ala Gly Ile Pro Asn Leu Asn Asp Val Arg Glu Leu Gly Ile  
275 280 285

Glu Phe Ile Thr Pro Ala Asn Ser Ser Gly Ser Phe Ala Ile Tyr Val  
290 295 300

Asp  
305

<210> 19  
<211> 397  
<212> DNA  
<213> Bacillus clausii

<400> 19  
atctctcagg gcttggtagg agtcattatt ctcttataca tggcatttag tcaagagaga 60  
ggattggcgc aaactggatt tcaagtaaca gggacccagt tgcttgatgg agagggcaat 120  
ccgtatgtga tgcgtggagt caatcacgga cattcatggt tcaaacaaga ccttgataca 180  
gcaataccag ctattgcagc gactggcgct aatacggatga gaatcgtttt atcgaatggc 240  
caacaatggg agcgagatac cgtagcggaa gttgaaagag tgcttgcagt taccgaagag 300  
gaaggcttga cggctgtact tgaagttcat gatgcgacgg gaagtgatga tccaaacgat 360  
ttgtttactg cagtggagta ttggtcagag agaggat 397

<210> 20  
<211> 132  
<212> PRT

<213> Bacillus clausii

<400> 20

Ile Ser Gln Gly Leu Val Gly Val Ile Ile Leu Leu Tyr Met Ala Phe  
1 5 10 15

Ser Gln Glu Arg Gly Leu Ala Gln Thr Gly Phe Gln Val Thr Gly Thr  
20 25 30

Gln Leu Leu Asp Gly Glu Gly Asn Pro Tyr Val Met Arg Gly Val Asn  
35 40 45

His Gly His Ser Trp Phe Lys Gln Asp Leu Asp Thr Ala Ile Pro Ala  
50 55 60

Ile Ala Ala Thr Gly Ala Asn Thr Val Arg Ile Val Leu Ser Asn Gly  
65 70 75 80

Gln Gln Trp Glu Arg Asp Thr Val Ala Glu Val Glu Arg Val Leu Ala  
85 90 95

Val Thr Glu Glu Glu Gly Leu Thr Ala Val Leu Glu Val His Asp Ala  
100 105 110

Thr Gly Ser Asp Asp Pro Asn Asp Leu Phe Thr Ala Val Glu Tyr Trp  
115 120 125

Ser Glu Arg Gly  
130

<210> 21

<211> 960

<212> DNA

<213> Bacillus sp.

<400> 21

atgaatcgta agcgggttaca atggggttga gcactagtgg tgggtgttggt tttgtttgta 60  
tacagtagcg gtttagcatc tgcacaaagc ggctttcacg taaaagggtac agagttgttg 120  
gacaaaaatg gcgatcctta cgttatgcgt ggcgtcaacc atggacattc ttggtttaa 180  
caagatttag aggaggcaat ccctgccata gcagaaacag gggcgaacac agtgagaatc 240  
gtcttatcca atggacagca atgggaaaaa gatgatgcct ctgagcttgc ccgtgtgctt 300  
gctgccacag aaacatatgg gttgacaacc gtgctggaag tccacgatgc tacaggaagt 360

gataatcccg atgatttaga taaagcagtc gattactgga tcgaaatggc tgatgttcta 420  
 aaggggacag aagaccgggt aatcattaac attgccaatg aatgggatgg ggcgtggagg 480  
 agtgacgttt gggcagaggc atacgcacaa gcgatcccg gcttgcgag tgctggcctc 540  
 gcccatacgt taatagttga tgcggcaggt tggggacagt accctgcctc tatccatgag 600  
 cggggagccg acgtatttgc ctccgatcca ttaaaaaaca caatgttttc catccatag 660  
 tacgaatatg caggagcgga tagggcgaca gtttctgaaa acatcgacgg tgtacttgct 720  
 gaaaatcttg ctgtggtaat cgggtgaattt ggccataggc atcatgatgg cgatgtcgat 780  
 gaagatgcga ttttggccta tacagcagag cggcaagtgg gctggcttgc ctggatcatg 840  
 tatggcaata gcgggggtgt tgaatacttg gatttaactg aaggcccatc aggtccatta 900  
 acgagttggg gcgaacggat tgtctatggg gaaatgggct taaaagtaat tgatcacttg 960

<210> 22  
 <211> 320  
 <212> PRT  
 <213> Bacillus sp.

<400> 22

Met Asn Arg Lys Arg Leu Gln Trp Val Gly Ala Leu Val Val Val Leu  
1 5 10 15

Val Leu Phe Val Tyr Ser Ser Gly Leu Ala Ser Ala Gln Ser Gly Phe  
20 25 30

His Val Lys Gly Thr Glu Leu Leu Asp Lys Asn Gly Asp Pro Tyr Val  
35 40 45

Met Arg Gly Val Asn His Gly His Ser Trp Phe Lys Gln Asp Leu Glu  
50 55 60

Glu Ala Ile Pro Ala Ile Ala Glu Thr Gly Ala Asn Thr Val Arg Ile  
65 70 75 80

Val Leu Ser Asn Gly Gln Gln Trp Glu Lys Asp Asp Ala Ser Glu Leu  
85 90 95

Ala Arg Val Leu Ala Ala Thr Glu Thr Tyr Gly Leu Thr Thr Val Leu  
100 105 110

Glu Val His Asp Ala Thr Gly Ser Asp Asn Pro Asp Asp Leu Asp Lys  
115 120 125

Ala Val Asp Tyr Trp Ile Glu Met Ala Asp Val Leu Lys Gly Thr Glu  
130 135 140

Asp Arg Val Ile Ile Asn Ile Ala Asn Glu Trp Tyr Gly Ala Trp Arg  
145 150 155 160

Ser Asp Val Trp Ala Glu Ala Tyr Ala Gln Ala Ile Pro Arg Leu Arg  
165 170 175

Ser Ala Gly Leu Ala His Thr Leu Ile Val Asp Ala Ala Gly Trp Gly  
180 185 190

Gln Tyr Pro Ala Ser Ile His Glu Arg Gly Ala Asp Val Phe Ala Ser  
195 200 205

Asp Pro Leu Lys Asn Thr Met Phe Ser Ile His Met Tyr Glu Tyr Ala  
210 215 220

Gly Ala Asp Arg Ala Thr Val Ser Glu Asn Ile Asp Gly Val Leu Ala  
225 230 235 240

Glu Asn Leu Ala Val Val Ile Gly Glu Phe Gly His Arg His His Asp  
245 250 255

Gly Asp Val Asp Glu Asp Ala Ile Leu Ala Tyr Thr Ala Glu Arg Gln  
260 265 270

Val Gly Trp Leu Ala Trp Ser Trp Tyr Gly Asn Ser Gly Gly Val Glu  
275 280 285

Tyr Leu Asp Leu Thr Glu Gly Pro Ser Gly Pro Leu Thr Ser Trp Gly  
290 295 300

Glu Arg Ile Val Tyr Gly Glu Met Gly Leu Lys Val Ile Asp His Leu  
305 310 315 320

<210> 23  
<211> 564  
<212> DNA  
<213> Bacillus sp.

<400> 23  
 atgaatcgta agcgggttaca atggggttga gcactagtgg cgggtgttgggt tttgtttgta 60  
 tacagtagcg gtttagcatc tgcacaaagc ggctttcacg taaaagggtac agagttgttg 120  
 gacaaaaatg gcgataccta cgttatgcgt ggcgtcaacc atggacattc ttggtttaaa 180  
 caagatttag aggaggcaat ccctgccata gcagaaacag gggcgaacac agtgagaatc 240  
 gtcttatcca atggacagca atgggaaaaa gatgatgcct ctgagcttgc ccgtgtgctt 300  
 gctgccacag aaacatatgg gttgacaacc gtgctggaag tccacgatgc tacaggaagt 360  
 gataatcccg atgatttaga taaagcagtc gattactgga tcgaaatggc tgatgttcta 420  
 aaggggacag aagaccgggt aatcattaac attgccaatg aatgggtatgg ggcgtggagg 480  
 agtgaccttt gggcaaaaagc atacgcacaa gcgatccgc gcttgccgag tgctggcctc 540  
 gcccatagct taataattga tgcc 564

<210> 24  
 <211> 188  
 <212> PRT  
 <213> Bacillus sp.

<400> 24

Met Asn Arg Lys Arg Leu Gln Trp Val Gly Ala Leu Val Ala Val Leu  
 1 5 10 15

Val Leu Phe Val Tyr Ser Ser Gly Leu Ala Ser Ala Gln Ser Gly Phe  
 20 25 30

His Val Lys Gly Thr Glu Leu Leu Asp Lys Asn Gly Asp Pro Tyr Val  
 35 40 45

Met Arg Gly Val Asn His Gly His Ser Trp Phe Lys Gln Asp Leu Glu  
 50 55 60

Glu Ala Ile Pro Ala Ile Ala Glu Thr Gly Ala Asn Thr Val Arg Ile  
 65 70 75 80

Val Leu Ser Asn Gly Gln Gln Trp Glu Lys Asp Asp Ala Ser Glu Leu  
 85 90 95

Ala Arg Val Leu Ala Ala Thr Glu Thr Tyr Gly Leu Thr Thr Val Leu  
 100 105 110



Glu Val His Asp Ala Thr Gly Ser Asp Asn Pro Asp Asp Leu Asp Lys  
 115 120 125

Ala Val Asp Tyr Trp Ile Glu Met Ala Asp Val Leu Lys Gly Thr Glu  
 130 135 140

Asp Arg Val Ile Ile Asn Ile Ala Asn Glu Trp Tyr Gly Ala Trp Arg  
 145 150 155 160

Ser Asp Leu Trp Ala Lys Ala Tyr Ala Gln Ala Ile Pro Arg Leu Arg  
 165 170 175

Ser Ala Gly Leu Ala His Thr Leu Ile Ile Asp Ala  
 180 185

<210> 25  
 <211> 2445  
 <212> DNA  
 <213> Bacillus sp.

<400> 25  
 atgaacaaac aaccgttaaa gactgcattt attatgttgt tatgtagcgt gtttatgttt 60  
 caaagcctac cttactatgt gaacgctatc aatgaaggcg agagagaagc ttttgcaccc 120  
 gcagggagat atgatgctga acaggcgact acgacaggaa atgccgtatt cacgaccgag 180  
 cctgttgagg acggcgagta cgccggtccg ggctacattt ctttcttttc tgaagattcc 240  
 tcgccacctt cttcatcgac aacctttcac attcaggccg ataaaacgga gctctatcat 300  
 ttatctatcg gatactatgc tccatacggg aacaagggaa ccacaattct ggtgaacggg 360  
 gcaggtaacg gagagtttat gttgccagcg cccgaggacg gggcagtctc cgccgaagtg 420  
 gaaattagca aaatcctgct cgaagaagga aataatacga ttacattcac aagaggctgg 480  
 gggtattacg gcattgaata tattcgggtc gagccgggta atccaacgtt accgactata 540  
 tttattgaag cagaagaaga ttacgaagcg actggaaatg ttagcggtac caatgaaatc 600  
 gaaggttatt ccggagcagg ctatttggtc aaccaagagg ggacaattca ttggaatgta 660  
 acctcaccgg aaacctctat atatgaagta atcgttgcct atgcagctcc ttatggcgac 720  
 aaacaaacaa atctgacagt gaatggacag ggtaccgtca atcttgactt gaaagagaca 780  
 gaagtcttcg tggagttgaa tgtcggcatc gtaagtctca atgaaggcga aaacacacta 840  
 acactccata gtggttgggg atggtacaat atcgattata tcaagcttgt acctgtgggc 900  
 agttcggatc ccgaaccgca tcaggctcga aaaacactgg tgaatccgga cgcctcacct 960

gaggcaagag cgctaattaa ttatctcgta gaccagtacg ggaacaaaat tctatcaggt 1020  
 caaaccgagt tgaaagacgc caggtggatc catgaacagg tgggcaaata tcctgcggtt 1080  
 atggcagttg attttatgga ctacagcccc tcccgcgtag tgcattggcgc aactggaact 1140  
 gcggttgagg aagcgattga gtgggcagag atgggtggga tcattacctt cactggcat 1200  
 tggaacgcgc caaaggacct gcttaatgta cccggcaatg agtgggtggc cggtttttat 1260  
 acccgtgcca caacgtttga tgtggagtac gctttagaga accgggaatc tgaggatttc 1320  
 caattgttga ttagcgacat ggatgtgatc gccgagcaat tgaagcggct gcaggcagag 1380  
 aacatccctg tgttatggag accgcttcat gaggcggaag gcggctgggt ctggtggggc 1440  
 gccaaaggtc cagaggcggc aatagagctc tacaggctga tgtacgatcg ttacaccaat 1500  
 caccataaac taaacaattt gatatggatg tggaattcgg aagcggaga atggtatccg 1560  
 ggcgatgatg tcgtggacat gatcagtacc gatatttata atcctgtcgg agatttcagt 1620  
 cccagcatca acaagtatga gcatctaaag gaattggtac aggataagaa gctggttgcc 1680  
 ttgcctgaaa ccggcattat tccggatccc gatcagcttc agctgttcaa tgcgaactgg 1740  
 agttggttcg ccacctggac tggagactat atcagggacg gcatctccaa ccctatagaa 1800  
 cacctgcaaa aggtgtttca tcatgactac gtcacacccc tggatgaatt gccggagaac 1860  
 ctgtcccgtt acggattatc tgaaggagtc tggaagagcg acgccgatct atccgtaaaa 1920  
 acgaggacga cctccgaaat tacagtgaac tgggtcaaag ccattcaata tgattccgtt 1980  
 aatggctata aattaattaa agatgggtga gagaccgttt cagttgaagg cggcgtgcaa 2040  
 gagtatacct tcacaaattt attgccgggc acgcagtata cgataaaaagt agaggcactg 2100  
 gaccaggatg accgatggac cgccgacgga ccggtcgccg ttgtatctac attatccaac 2160  
 gctccgatat cctatcctcc ggctgtcact cctgatgagc cgaatgaaga actgtcggag 2220  
 ggagagtata cgctcttggc agatgactta tccagccagg atgggtgttct ggaagtaagt 2280  
 cttgagccga cagttacgaa gctcattatt ccttctgcac tagccggcac attagacgga 2340  
 gacttgagaa tcggttatgg ggacgtctgg atcgtcatcc cacacgaaca gcttgggggt 2400  
 gacgagcagc aatccggcag cgcgtatgag ttagtgctgg agatc 2445

<210> 26  
 <211> 815  
 <212> PRT  
 <213> Bacillus sp.

<400> 26

Met Asn Lys Gln Pro Leu Lys Thr Ala Phe Ile Met Leu Leu Cys Ser  
1 5 10 15

Val Phe Met Phe Gln Ser Leu Pro Tyr Tyr Val Asn Ala Ile Asn Glu  
20 25 30

Gly Glu Arg Glu Ala Phe Ala Ser Ala Gly Arg Tyr Asp Ala Glu Gln  
35 40 45

Ala Thr Thr Thr Gly Asn Ala Val Phe Thr Thr Glu Pro Val Glu Asp  
50 55 60

Gly Glu Tyr Ala Gly Pro Gly Tyr Ile Ser Phe Phe Ser Glu Asp Ser  
65 70 75 80

Ser Pro Pro Ser Ser Ser Thr Thr Phe His Ile Gln Ala Asp Lys Thr  
85 90 95

Glu Leu Tyr His Leu Ser Ile Gly Tyr Tyr Ala Pro Tyr Gly Asn Lys  
100 105 110

Gly Thr Thr Ile Leu Val Asn Gly Ala Gly Asn Gly Glu Phe Met Leu  
115 120 125

Pro Ala Pro Glu Asp Gly Ala Val Ser Ala Glu Val Glu Ile Ser Lys  
130 135 140

Ile Leu Leu Glu Glu Gly Asn Asn Thr Ile Thr Phe Thr Arg Gly Trp  
145 150 155 160

Gly Tyr Tyr Gly Ile Glu Tyr Ile Arg Val Glu Pro Val Asn Pro Thr  
165 170 175

Leu Pro Thr Ile Phe Ile Glu Ala Glu Glu Asp Tyr Glu Ala Thr Gly  
180 185 190

Asn Val Ser Val Thr Asn Glu Ile Glu Gly Tyr Ser Gly Ala Gly Tyr  
195 200 205

Leu Phe Asn Gln Glu Gly Thr Ile His Trp Asn Val Thr Ser Pro Glu  
210 215 220

Thr Ser Ile Tyr Glu Val Ile Val Ala Tyr Ala Ala Pro Tyr Gly Asp  
225 230 235 240

Lys Gln Thr Asn Leu Thr Val Asn Gly Gln Gly Thr Val Asn Leu Asp  
245 250 255

Leu Lys Glu Thr Glu Val Phe Val Glu Leu Asn Val Gly Ile Val Ser  
260 265 270

Leu Asn Glu Gly Glu Asn Thr Leu Thr Leu His Ser Gly Trp Gly Trp  
275 280 285

Tyr Asn Ile Asp Tyr Ile Lys Leu Val Pro Val Val Ser Ser Asp Pro  
290 295 300

Glu Pro His Gln Val Glu Lys Thr Leu Val Asn Pro Asp Ala Ser Pro  
305 310 315 320

Glu Ala Arg Ala Leu Ile Asn Tyr Leu Val Asp Gln Tyr Gly Asn Lys  
325 330 335

Ile Leu Ser Gly Gln Thr Glu Leu Lys Asp Ala Arg Trp Ile His Glu  
340 345 350

Gln Val Gly Lys Tyr Pro Ala Val Met Ala Val Asp Phe Met Asp Tyr  
355 360 365

Ser Pro Ser Arg Val Val His Gly Ala Thr Gly Thr Ala Val Glu Glu  
370 375 380

Ala Ile Glu Trp Ala Glu Met Gly Gly Ile Ile Thr Phe His Trp His  
385 390 395 400

Trp Asn Ala Pro Lys Asp Leu Leu Asn Val Pro Gly Asn Glu Trp Trp  
405 410 415

Ser Gly Phe Tyr Thr Arg Ala Thr Thr Phe Asp Val Glu Tyr Ala Leu  
420 425 430

Glu Asn Arg Glu Ser Glu Asp Phe Gln Leu Leu Ile Ser Asp Met Asp  
435 440 445

Val Ile Ala Glu Gln Leu Lys Arg Leu Gln Ala Glu Asn Ile Pro Val  
450 455 460

Leu Trp Arg Pro Leu His Glu Ala Glu Gly Gly Trp Phe Trp Trp Gly  
465 470 475 480

Ala Lys Gly Pro Glu Ala Ala Ile Glu Leu Tyr Arg Leu Met Tyr Asp  
485 490 495

Arg Tyr Thr Asn His His Lys Leu Asn Asn Leu Ile Trp Met Trp Asn  
500 505 510

Ser Glu Ala Glu Glu Trp Tyr Pro Gly Asp Asp Val Val Asp Met Ile  
515 520 525

Ser Thr Asp Ile Tyr Asn Pro Val Gly Asp Phe Ser Pro Ser Ile Asn  
530 535 540

Lys Tyr Glu His Leu Lys Glu Leu Val Gln Asp Lys Lys Leu Val Ala  
545 550 555 560

Leu Pro Glu Thr Gly Ile Ile Pro Asp Pro Asp Gln Leu Gln Leu Phe  
565 570 575

Asn Ala Asn Trp Ser Trp Phe Ala Thr Trp Thr Gly Asp Tyr Ile Arg  
580 585 590

Asp Gly Ile Ser Asn Pro Ile Glu His Leu Gln Lys Val Phe His His  
595 600 605

Asp Tyr Val Ile Thr Leu Asp Glu Leu Pro Glu Asn Leu Ser Arg Tyr  
610 615 620

Gly Leu Ser Glu Gly Val Trp Lys Ser Asp Ala Asp Leu Ser Val Lys  
625 630 635 640

Thr Arg Thr Thr Ser Glu Ile Thr Val Asn Trp Ser Asn Ala Ile Gln  
645 650 655

Tyr Asp Ser Val Asn Gly Tyr Lys Leu Ile Lys Asp Gly Val Glu Thr  
660 665 670

Val Ser Val Glu Gly Gly Val Gln Glu Tyr Thr Phe Thr Asn Leu Leu

675

680

685

Pro Gly Thr Gln Tyr Thr Ile Lys Val Glu Ala Leu Asp Gln Asp Asp  
690 695 700

Arg Trp Thr Ala Asp Gly Pro Val Ala Val Val Ser Thr Leu Ser Asn  
705 710 715 720

Ala Pro Ile Ser Tyr Pro Pro Ala Val Thr Pro Asp Glu Pro Asn Glu  
725 730 735

Glu Leu Ser Glu Gly Glu Tyr Thr Leu Leu Ala Asp Asp Leu Ser Ser  
740 745 750

Gln Asp Gly Val Leu Glu Val Ser Leu Glu Pro Thr Val Thr Lys Leu  
755 760 765

Ile Ile Pro Ser Ala Leu Ala Gly Thr Leu Asp Gly Asp Leu Arg Ile  
770 775 780

Gly Tyr Gly Asp Val Trp Ile Val Ile Pro His Glu Gln Leu Gly Gly  
785 790 795 800

Asp Glu Gln Gln Ser Gly Ser Ala Tyr Glu Leu Val Leu Glu Ile  
805 810 815

<210> 27

<211> 1488

<212> DNA

<213> Bacillus sp.

<400> 27

atgaggaatg aaaaaatcag gccatttact aaaataaagg caagtgttgt tactagtgtt 60  
ttactatttaa ctatttcctt aattttcact ataggaaata tagcaaagtc tgaatctgag 120  
gtaagaatat ttgaagctga agatgctatt ttaaagggc tgactattaa aaattctgaa 180  
ccagggtttt ctggtaccgg atatgtaggt gactttgaaa atagctctca gagtgtgacg 240  
tttcaaattg aggctcctaa agccggttta tacaacttaa atattggata tggcgcgatt 300  
tatggaagtg gaaaagtagc taatgttatt gtaaagggag agaagctaag tacttttaca 360  
atgggaagtg gctttggtaa agcgtcagca ggaaaggtat tacttaattc aggcttaaat 420  
actatctcga ttactcctaa ttggacatgg tttaccattg attatattga agttatacat 480

gcaccggaac cggaaaacca taatgtagaa aagacgttaa ttaacccaaa tgcaacggat 540  
gaagccaaag ctttaataag ctatctagtt gataactttg gtgagaaaat tcttgagg 600  
caacatgatt atccaaatac acgaccacga gatttagaat atatttatga aactactggg 660  
aagtatcctg ctgttttagg tttagacttt attgataaca gtccttctag agttgagcgc 720  
ggagcctctg ctgatgaaac accagtagct attgactggg ggaataaagg gggaattgtt 780  
actttcacct ggcattggaa tgctcccaa gatttattag atgaaccagg aaatgaatgg 840  
tgagtggtt tttatacgag agcaacaact tttgacgtag aatatgcttt aaaacatccg 900  
aagtcggagg actacatgct tctaatacgt gatattgatg taatagctgg tgaactaaag 960  
aaattgcagg aagcaaatgt tcctgtttta tggaggccac ttcattgagg tgaaggcggg 1020  
tggttctggt ggggggcaaa aggtcctgaa tcaaccaagg agctatggag attaatgtat 1080  
gatagaatga cgaactacca taacttaaat aatttaatat gggatatggaa ttccattgaa 1140  
gaggattggt atcctggaga tgagtatgtc gatattgtaa gcttcgattc atatccagg 1200  
gaatataact atagtccaat gagccgtgag tatgaagcac ttaaagagtt gtctagtaac 1260  
aagaaactta tagcaatagc agaaaatgga ccaataccag atcctgattt actacaactt 1320  
taccatgcta actatagttg gtttgctaca tggaatggag atatattaag aaatcaaaat 1380  
agcgaagagc acctaagaaa agtatataat catgattatg tgattaccct aaataaatta 1440  
cctaacctta aaacatatag gggaagatgc acttatacag acactatc 1488

<210> 28  
<211> 496  
<212> PRT  
<213> Bacillus sp.

<400> 28

Met Arg Asn Glu Lys Ile Arg Pro Phe Thr Lys Ile Lys Ala Ser Val  
1 5 10 15

Val Thr Ser Val Leu Leu Leu Thr Ile Ser Leu Ile Phe Thr Ile Gly  
20 25 30

Asn Ile Ala Asn Ala Glu Ser Glu Val Arg Ile Phe Glu Ala Glu Asp  
35 40 45

Ala Ile Leu Asn Gly Leu Thr Ile Lys Asn Ser Glu Pro Gly Phe Ser  
50 55 60

Gly Thr Gly Tyr Val Gly Asp Phe Glu Asn Ser Ser Gln Ser Val Thr  
65 70 75 80

Phe Gln Ile Glu Ala Pro Lys Ala Gly Leu Tyr Asn Leu Asn Ile Gly  
85 90 95

Tyr Gly Ala Ile Tyr Gly Ser Gly Lys Val Ala Asn Val Ile Val Asn  
100 105 110

Gly Glu Lys Leu Ser Thr Phe Thr Met Gly Ser Gly Phe Gly Lys Ala  
115 120 125

Ser Ala Gly Lys Val Leu Leu Asn Ser Gly Leu Asn Thr Ile Ser Ile  
130 135 140

Thr Pro Asn Trp Thr Trp Phe Thr Ile Asp Tyr Ile Glu Val Ile His  
145 150 155 160

Ala Pro Glu Pro Glu Asn His Asn Val Glu Lys Thr Leu Ile Asn Pro  
165 170 175

Asn Ala Thr Asp Glu Ala Lys Ala Leu Ile Ser Tyr Leu Val Asp Asn  
180 185 190

Phe Gly Glu Lys Ile Leu Ala Gly Gln His Asp Tyr Pro Asn Thr Arg  
195 200 205

Pro Arg Asp Leu Glu Tyr Ile Tyr Glu Thr Thr Gly Lys Tyr Pro Ala  
210 215 220

Val Leu Gly Leu Asp Phe Ile Asp Asn Ser Pro Ser Arg Val Glu Arg  
225 230 235 240

Gly Ala Ser Ala Asp Glu Thr Pro Val Ala Ile Asp Trp Trp Asn Lys  
245 250 255

Gly Gly Ile Val Thr Phe Thr Trp His Trp Asn Ala Pro Lys Asp Leu  
260 265 270

Leu Asp Glu Pro Gly Asn Glu Trp Trp Ser Gly Phe Tyr Thr Arg Ala  
275 280 285



Thr Thr Phe Asp Val Glu Tyr Ala Leu Lys His Pro Lys Ser Glu Asp  
290 295 300

Tyr Met Leu Leu Ile Arg Asp Ile Asp Val Ile Ala Gly Glu Leu Lys  
305 310 315 320

Lys Leu Gln Glu Ala Asn Val Pro Val Leu Trp Arg Pro Leu His Glu  
325 330 335

Ala Glu Gly Gly Trp Phe Trp Trp Gly Ala Lys Gly Pro Glu Ser Thr  
340 345 350

Lys Glu Leu Trp Arg Leu Met Tyr Asp Arg Met Thr Asn Tyr His Asn  
355 360 365

Leu Asn Asn Leu Ile Trp Val Trp Asn Ser Ile Glu Glu Asp Trp Tyr  
370 375 380

Pro Gly Asp Glu Tyr Val Asp Ile Val Ser Phe Asp Ser Tyr Pro Gly  
385 390 395 400

Glu Tyr Asn Tyr Ser Pro Met Ser Arg Glu Tyr Glu Ala Leu Lys Glu  
405 410 415

Leu Ser Ser Asn Lys Lys Leu Ile Ala Ile Ala Glu Asn Gly Pro Ile  
420 425 430

Pro Asp Pro Asp Leu Leu Gln Leu Tyr His Ala Asn Tyr Ser Trp Phe  
435 440 445

Ala Thr Trp Asn Gly Asp Ile Leu Arg Asn Gln Asn Ser Glu Glu His  
450 455 460

Leu Arg Lys Val Tyr Asn His Asp Tyr Val Ile Thr Leu Asn Lys Leu  
465 470 475 480

Pro Asn Leu Lys Thr Tyr Arg Gly Arg Cys Thr Tyr Thr Asp Thr Ile  
485 490 495

<210> 29  
<211> 1086  
<212> DNA  
<213> Bacillus licheniformis

41 248

e

<400> 29  
atgtacaaaa aatttggaat ctctttattg cttgctttat taatcgtttc agctttctcg 60  
cagacggcat ctgctcatac agtgaatccg gtgaaccaa atgcccagtc gacaacgaag 120  
gagctgatga attggcttgc tcatctgccg aaccgatcgg aaaatcgcg actgtcaggt 180  
gcattcggcg gatattctaa tgcgacgttt tctatgaaag aagccaatcg aatcaaagat 240  
gctacagggc agtcacctgt cgtgtatgct tgtgattatt cgagaggatg gctggagaca 300  
gctcatattg ctgatgcat cgattatagc tgtaacagcg atctaatttc tcattggaag 360  
agcggaggca tacctcagat cagcatgcat cttcctaacc ctgctgttca atccggcaat 420  
tacaaaacaa agatctcaaa cagtcagtat gaaaaaatct tagactcatc aaccacagaa 480  
ggcaaacgat tggatgctgt actgagcaag gttgcagatg gccttcagca gttaaaaaat 540  
gaaggcggtc cagttctttt cagacctctt cacgaaatga acggagaatg gttctgggtg 600  
gggcttaccg gctataacca aaaggatagc gagcgaatat cactatacaa acagctttac 660  
caaaaaatct atcattatat gaccgatata agaggattgg acaacttgat ttgggtttat 720  
gcaccagacg ccaaccgcga ctttaagaca gacttttatc ctggggattc atatgttgat 780  
attgtcggat tagacgcgta tttctcagat gcttattcga tcaaaggata tgacgagtta 840  
acggcgctta ataagccatt tgcctttaca gaagtcggtc cgcaaacaac aaacggcagc 900  
ctggattatt ctcaatttat caatgcagtt aaacaaaaat atccgaaaac catttatttc 960  
ttagcttggg atgaggggtg gagccctgcg gctaatacagg gtgcctttaa tctctataat 1020  
gacagttgga cgctgaataa gggagagcta tgggaaggca gctcacttac accggcagcc 1080  
gaataa 1086

<210> 30  
<211> 361  
<212> PRT  
<213> Bacillus licheniformis

<400> 30

Met Tyr Lys Lys Phe Gly Ile Ser Leu Leu Leu Ala Leu Leu Ile Val  
1 5 10 15

Ser Ala Phe Ser Gln Thr Ala Ser Ala His Thr Val Asn Pro Val Asn  
20 25 30

Gln Asn Ala Gln Ser Thr Thr Lys Glu Leu Met Asn Trp Leu Ala His  
35 40 45

Leu Pro Asn Arg Ser Glu Asn Arg Val Leu Ser Gly Ala Phe Gly Gly  
50 55 60

Tyr Ser Asn Ala Thr Phe Ser Met Lys Glu Ala Asn Arg Ile Lys Asp  
65 70 75 80

Ala Thr Gly Gln Ser Pro Val Val Tyr Ala Cys Asp Tyr Ser Arg Gly  
85 90 95

Trp Leu Glu Thr Ala His Ile Ala Asp Ala Ile Asp Tyr Ser Cys Asn  
100 105 110

Ser Asp Leu Ile Ser His Trp Lys Ser Gly Gly Ile Pro Gln Ile Ser  
115 120 125

Met His Leu Pro Asn Pro Ala Phe Gln Ser Gly Asn Tyr Lys Thr Lys  
130 135 140

Ile Ser Asn Ser Gln Tyr Glu Lys Ile Leu Asp Ser Ser Thr Thr Glu  
145 150 155 160

Gly Lys Arg Leu Asp Ala Val Leu Ser Lys Val Ala Asp Gly Leu Gln  
165 170 175

Gln Leu Lys Asn Glu Gly Val Pro Val Leu Phe Arg Pro Leu His Glu  
180 185 190

Met Asn Gly Glu Trp Phe Trp Trp Gly Leu Thr Gly Tyr Asn Gln Lys  
195 200 205

Asp Ser Glu Arg Ile Ser Leu Tyr Lys Gln Leu Tyr Gln Lys Ile Tyr  
210 215 220

His Tyr Met Thr Asp Thr Arg Gly Leu Asp Asn Leu Ile Trp Val Tyr  
225 230 235 240

Ala Pro Asp Ala Asn Arg Asp Phe Lys Thr Asp Phe Tyr Pro Gly Asp  
245 250 255

Ser Tyr Val Asp Ile Val Gly Leu Asp Ala Tyr Phe Ser Asp Ala Tyr  
260 265 270

Ser Ile Lys Gly Tyr Asp Glu Leu Thr Ala Leu Asn Lys Pro Phe Ala  
 275 280 285

Phe Thr Glu Val Gly Pro Gln Thr Thr Asn Gly Ser Leu Asp Tyr Ser  
 290 295 300

Gln Phe Ile Asn Ala Val Lys Gln Lys Tyr Pro Lys Thr Ile Tyr Phe  
 305 310 315 320

Leu Ala Trp Asp Glu Gly Trp Ser Pro Ala Ala Asn Gln Gly Ala Phe  
 325 330 335

Asn Leu Tyr Asn Asp Ser Trp Thr Leu Asn Lys Gly Glu Leu Trp Glu  
 340 345 350

Gly Ser Ser Leu Thr Pro Ala Ala Glu  
 355 360

<210> 31  
 <211> 3041  
 <212> DNA  
 <213> Caldocellulosiruptor sp.

<400> 31  
 caatgggctt gaagattggt attcactggg gtgctgattt tgtaatagcc aatatcaagg 60  
 ttgaagaggt aactcagtaa aagaggcttt ttgctgggtga gcacaccgct gaagagaaaa 120  
 gtaagggttat gttaaagaag cgggtgtgcc accggcttta aaaaaataaa aaaggggaga 180  
 gtgccaggat tatgagaaaag ggcttaaaga ttacatcttt aatagtgagc cttgtatttt 240  
 tacttgggct tttgccgaca ggaatttttg gtgctgttga gacatctgtt caaagctatg 300  
 ttttcgactt tgaagatggc accacaatga cattcgggtga ggcttgggga gactcattaa 360  
 aatgtatcaa aaagggtgtca gtttctactg atttgcagcg acctggtaac aagtatgcgc 420  
 tcaggcttga tggtgagttc aacgagaaca atggatggga ccagggcgac cttggtgcat 480  
 ggataggtgg tggtgtcgaa gggcagtttg actttacaaa ctacaagtct gttgagtttg 540  
 aaatgtttgt tccatacgac gagtttgcaa aagcaaaagg tggctttgct tacaagggtg 600  
 tattgaatga tggatggaaa gaacttgga gcaatttag cattacagta aatgctggca 660  
 aaaagggtgaa gataaacggc aaggactata tggtcattca caaggcgttt gcaattccag 720  
 atgatttttag aacccaaaaag cgtgcacagc ttgtgttcca atttgcaggt caaaactgca 780

actacaaagg acctatctac cttgacaata taagagtaag acctgaggat gcgtcaaacc 840  
tctcaaaaga agactatgga agtagcgaag aagaggaaat ttctgaggac tttttcacag 900  
gggttacct tgtgtatcca caggaaggca aaaactttgt gtacaatttt gaaaaagaca 960  
caatgggatt ttataaatac tcgggtgatg gatttgcaaa gaaaacaaag tcaatggaat 1020  
tttcacagga cttgaagaca tcaacaaatg caggcagcct caaactcaat gctaattttcc 1080  
agggtactgc gtttgaagaa atgaacattg ctgtaaagct cacagacaaa gaaggaaaac 1140  
tttttgacct tggcaaatac tccgcacttg agtatacaat ctacattcca aatccagaca 1200  
aagttgcggg gaaaatcatg tctgcaagtg ctgtggacag tccatggaag ataatcaaag 1260  
actttacact tcttaactac aaagataaga caacatggaa agagataaac ggaaagactt 1320  
atgcggtcat aaagtgaag gataatcttt acaatgtaaa agaaaaagca ggtgtattgg 1380  
ttttgaggat tgcgggggtct tatgtaaagt atacaggccc catctacatt gataacgtaa 1440  
cattaattgc tggaaagaag gttgcaccaa aggtggagag aatatcactt ccaaatccaa 1500  
agacatacta taaagttaag attgaagctg agagtgaag tgatggctgg gcttacagcg 1560  
ttgagaaaaga aaatgcaaag ttttctggga aaggctatgt acttttgttt gggaacaaca 1620  
tgggcaatac cctttataac atcaagggtc cgaagacagg acattacatc ttcactcttg 1680  
caatctcaac ccttgggctt gtaaaggatg gtagcattga tatctggata gacggtgatt 1740  
tgaaagggtg ggcaaagggt ccaaacgtaa agggcaagtt ccaggaagtt gttgtcagaa 1800  
aaaagattta tttaacagcg ggtgagcaca caatatcact gcaaaaatct ggcggataca 1860  
caattgcagt tgactatttt gtgatagaag agcttggtgc ggcaaataaa tcaaagcttt 1920  
cggtttcttc aaagttagtg accccaaatc cacaccccaa tgcccaaagg ctcataaatt 1980  
atgtgtcaag catttacggt gaaaagattt tgtctggtca gcagagcagc ggtgaaggca 2040  
aagaggttca gatgattttt gatgtcaca agagatatcc agctgttaga agctttgatt 2100  
tcatggacta ctcaccaagc agagtgcagc atggtacaaa aggtacagat gttgatgagg 2160  
caataaagtg gtggaagagc ggcggcatag ttgcattttg ctggcactgg aacgcaccaa 2220  
caggtcttat tgaccagccg ggcaaagagt ggtggagagg tttttacaca gaggctacaa 2280  
catttgacct caagaaagcc atggacaatc caaattctga agaataaaa ctcattttga 2340  
gagatataga cgctattgct gagcagctca aaaaattgca ggctgaagggt gtgccagttc 2400  
ttttcagacc gcttcacgag gcctctggcg gctgggtctg gtgggggtgca aaagggtccag 2460  
agccgtatat aaagcttttg aagctcatgt ttgacaggct tgtaaactat cacaaaatca 2520

acaaccta atgggtatg aacggtcagg atgctgcctg gstatccgggt gaccagtatg 2580  
 ttgatataat tgcagaagat atatatgagg aaaaagctca gtactcacca tatacagaga 2640  
 gggtcgtgaa agctctcaag tacacaaatg caaacaagat gatagcactt tctgagtgcg 2700  
 gaactattcc tgacccgggt gtgctaaaac aagaagggtg ttcgtggctg tggttttctg 2760  
 tatgggcagg aagctatgtc atgacaggca gcaagtacaa cgatgaatgg aacgacaatc 2820  
 acatgctaag aaagatttac aacaatgact atgtaataac aaaagatgaa ctacctgata 2880  
 taaagagcat tccactcaaa tagaatgaga tatattttgg aatatccaaa atcaactgtc 2940  
 agcctgtgag aggagagaag ttcaaaaaag acctcctccc tttttgggtc ttgcaaaata 3000  
 atcaattttt ggttttgaca tctcaaacat gttaattaaa a 3041

<210> 32  
 <211> 903  
 <212> PRT  
 <213> Caldocellulosiruptor sp.

<400> 32

Met Arg Lys Gly Leu Lys Ile Thr Ser Leu Ile Val Ser Leu Val Phe  
1 5 10 15

Leu Leu Gly Leu Leu Pro Thr Gly Ile Phe Gly Ala Val Glu Thr Ser  
20 25 30

Val Gln Ser Tyr Val Phe Asp Phe Glu Asp Gly Thr Thr Met Thr Phe  
35 40 45

Gly Glu Ala Trp Gly Asp Ser Leu Lys Cys Ile Lys Lys Val Ser Val  
50 55 60

Ser Thr Asp Leu Gln Arg Pro Gly Asn Lys Tyr Ala Leu Arg Leu Asp  
65 70 75 80

Val Glu Phe Asn Glu Asn Asn Gly Trp Asp Gln Gly Asp Leu Gly Ala  
85 90 95

Trp Ile Gly Gly Val Val Glu Gly Gln Phe Asp Phe Thr Asn Tyr Lys  
100 105 110

Ser Val Glu Phe Glu Met Phe Val Pro Tyr Asp Glu Phe Ala Lys Ala  
115 120 125

Lys Gly Gly Phe Ala Tyr Lys Val Val Leu Asn Asp Gly Trp Lys Glu  
130 135 140

Leu Gly Ser Glu Phe Ser Ile Thr Val Asn Ala Gly Lys Lys Val Lys  
145 150 155 160

Ile Asn Gly Lys Asp Tyr Met Val Ile His Lys Ala Phe Ala Ile Pro  
165 170 175

Asp Asp Phe Arg Thr Lys Lys Arg Ala Gln Leu Val Phe Gln Phe Ala  
180 185 190

Gly Gln Asn Cys Asn Tyr Lys Gly Pro Ile Tyr Leu Asp Asn Ile Arg  
195 200 205

Val Arg Pro Glu Asp Ala Ser Asn Leu Ser Lys Glu Asp Tyr Gly Ser  
210 215 220

Ser Glu Glu Glu Glu Ile Ser Glu Asp Phe Phe Thr Gly Val Thr Leu  
225 230 235 240

Val Tyr Pro Gln Glu Gly Lys Asn Phe Val Tyr Asn Phe Glu Lys Asp  
245 250 255

Thr Met Gly Phe Tyr Lys Tyr Ser Gly Asp Gly Phe Ala Lys Lys Thr  
260 265 270

Lys Ser Met Glu Phe Ser Gln Asp Leu Lys Thr Ser Thr Asn Ala Gly  
275 280 285

Ser Leu Lys Leu Asn Ala Asn Phe Gln Gly Thr Ala Phe Glu Glu Met  
290 295 300

Asn Ile Ala Val Lys Leu Thr Asp Lys Glu Gly Lys Leu Phe Asp Leu  
305 310 315 320

Gly Lys Tyr Ser Ala Leu Glu Tyr Thr Ile Tyr Ile Pro Asn Pro Asp  
325 330 335

Lys Val Ala Gly Lys Ile Met Ser Ala Ser Ala Val Asp Ser Pro Trp  
340 345 350

47 254

E

Lys Ile Ile Lys Asp Phe Thr Leu Leu Asn Tyr Lys Asp Lys Thr Thr  
355 360 365

Trp Lys Glu Ile Asn Gly Lys Thr Tyr Ala Val Ile Lys Cys Lys Asp  
370 375 380

Asn Leu Tyr Asn Val Lys Glu Lys Ala Gly Val Leu Val Leu Arg Ile  
385 390 395 400

Ala Gly Ser Tyr Val Lys Tyr Thr Gly Pro Ile Tyr Ile Asp Asn Val  
405 410 415

Thr Leu Ile Ala Gly Lys Lys Val Ala Pro Lys Val Glu Arg Ile Ser  
420 425 430

Leu Pro Asn Pro Lys Thr Tyr Tyr Lys Val Lys Ile Glu Ala Glu Ser  
435 440 445

Ala Ser Asp Gly Trp Ala Tyr Ser Val Glu Lys Glu Asn Ala Lys Phe  
450 455 460

Ser Gly Lys Gly Tyr Val Leu Leu Phe Gly Asn Asn Met Gly Asn Thr  
465 470 475 480

Leu Tyr Asn Ile Lys Val Pro Lys Thr Gly His Tyr Ile Phe Thr Leu  
485 490 495

Ala Ile Ser Thr Leu Gly Leu Val Lys Asp Gly Ser Ile Asp Ile Trp  
500 505 510

Ile Asp Gly Asp Leu Lys Gly Gly Ala Lys Val Pro Asn Val Lys Gly  
515 520 525

Lys Phe Gln Glu Val Val Val Arg Lys Lys Ile Tyr Leu Thr Ala Gly  
530 535 540

Glu His Thr Ile Ser Leu Gln Lys Ser Gly Gly Tyr Thr Ile Ala Val  
545 550 555 560

Asp Tyr Phe Val Ile Glu Glu Leu Val Ala Ala Asn Lys Ser Lys Leu  
565 570 575



Ser Val Ser Ser Lys Leu Val Thr Pro Asn Pro His Pro Asn Ala Gln  
580 585 590

Arg Leu Ile Asn Tyr Leu Ser Ser Ile Tyr Gly Glu Lys Ile Leu Ser  
595 600 605

Gly Gln Gln Ser Ser Gly Glu Gly Lys Glu Val Gln Met Ile Phe Asp  
610 615 620

Val Thr Lys Arg Tyr Pro Ala Val Arg Ser Phe Asp Phe Met Asp Tyr  
625 630 635 640

Ser Pro Ser Arg Val Gln His Gly Thr Lys Gly Thr Asp Val Asp Glu  
645 650 655

Ala Ile Lys Trp Trp Lys Ser Gly Gly Ile Val Ala Phe Cys Trp His  
660 665 670

Trp Asn Ala Pro Thr Gly Leu Ile Asp Gln Pro Gly Lys Glu Trp Trp  
675 680 685

Arg Gly Phe Tyr Thr Glu Ala Thr Thr Phe Asp Leu Lys Lys Ala Met  
690 695 700

Asp Asn Pro Asn Ser Glu Glu Tyr Lys Leu Ile Leu Arg Asp Ile Asp  
705 710 715 720

Ala Ile Ala Glu Gln Leu Lys Lys Leu Gln Ala Glu Gly Val Pro Val  
725 730 735

Leu Phe Arg Pro Leu His Glu Ala Ser Gly Gly Trp Phe Trp Trp Gly  
740 745 750

Ala Lys Gly Pro Glu Pro Tyr Ile Lys Leu Trp Lys Leu Met Phe Asp  
755 760 765

Arg Leu Val Asn Tyr His Lys Ile Asn Asn Leu Ile Trp Val Trp Asn  
770 775 780

Gly Gln Asp Ala Ala Trp Tyr Pro Gly Asp Gln Tyr Val Asp Ile Ile  
785 790 795 800

Ala Glu Asp Ile Tyr Glu Glu Lys Ala Gln Tyr Ser Pro Tyr Thr Glu

805

810

815

Arg Phe Val Lys Ala Leu Lys Tyr Thr Asn Ala Asn Lys Met Ile Ala  
820 825 830

Leu Ser Glu Cys Gly Thr Ile Pro Asp Pro Ala Val Leu Lys Gln Glu  
835 840 845

Gly Val Ser Trp Leu Trp Phe Ser Val Trp Ala Gly Ser Tyr Val Met  
850 855 860

Thr Gly Ser Lys Tyr Asn Asp Glu Trp Asn Asp Asn His Met Leu Arg  
865 870 875 880

Lys Ile Tyr Asn Asn Asp Tyr Val Ile Thr Lys Asp Glu Leu Pro Asp  
885 890 895

Ile Lys Ser Ile Pro Leu Lys  
900

<210> 33

<211> 1450

<212> RNA

<213> Bacillus sp. I633

<400> 33

|   |     |
|---|-----|
| gcucccugau guuagcggcg gacgggugag uaacacgugg gcaaccugcc cuguagacug | 60  |
| ggauaacauc gagaaucgg ugcuaauacc ggauaauga uggaauugca uaaauucuaau  | 120 |
| uuaaaagaug gcuccggcua ucacuacagg augggcccg gcgcgaauag cuaguuggua  | 180 |
| agguaacggc uuaccaaggc gacgaugcgu agccgaccug agagggugau cggccacacu | 240 |
| gggacugaga cacggcccag acuccuacgg gaggcagcag uagggaaucu uccgcaaugg | 300 |
| acgaaagucu gacggagcaa cgccgcguga gcgaugaagg ccuucggguu guaaagcucu | 360 |
| guuguuaggg aagaacaagu gccauucaa uaggguggca ccuugacggu accuaaccag  | 420 |
| aaagccacgg cuaacuacgu gccagcagcc gcgguaauac guagguggca agcguugucc | 480 |
| ggaaauauug ggcguaaagc gcgcgcaggc gguuucuaa gucugaugug aaagcccccg  | 540 |
| gcucaaccgg ggagggucau uggaacugg gagacuugag uacagaagag gagaguggaa  | 600 |
| uuccacgugu agcggugaaa ugcguagaua uguggaggaa caccaguggc gaaggcgacu | 660 |
| cucuggucug uaacugacgc ugaggcgca aagcgugggg agcaaacagg auuagauacc  | 720 |

50  
257

E

cugguagucc acgccguaaa cgaugagugc uagguguuag ggguuucgau gcccuuagug 780  
 ccgaaguuua cacaguaagc acuccgccug gggaguacgg ccgcaaggcu gaaacucaaa 840  
 ggaaauagacg ggggcccgc caagcggugg agcauguggu uuaauucgaa gcaacgcgaa 900  
 gaaccuuacc aggucuugac auccuuugac aacccuagag auagggcgau ccccuucggg 960  
 ggacaaaagug acagguggug caugguuguc gucagcucgu gucgugagau guuggguuaa 1020  
 gucccgcac gagcgcaacc cuugaucua guugccagca uuuauguagg cacucuaagg 1080  
 ugacugccgg ugacaaaccg gaggaaggug gggauagcgu caaaucaca ugccccuuau 1140  
 gaccugggcu acacacgugc uacaauggau gguacaaagg gcagcaaac cgcgaggugc 1200  
 agccaaucac auaaaaccu ucucaguucg gauuguaggc ugcaacucgc cuacaugaag 1260  
 ccggaaucgc uaguaaucgc ggaucagcau gccgcgguga auacguuccc gggccuugua 1320  
 cacaccgccc gucacaccac gagaguuuu aacacccgaa gucggugggg uaaccuuuug 1380  
 gagccagccg ccuaaggugg gacagaugau uggggugaag ucguaacaag guagccguau 1440  
 cggaaggugc 1450

<210> 34  
 <211> 1508  
 <212> RNA  
 <213> Bacillus sp. AAI12

<400> 34  
 gacgaacgcu ggcggcgugc cuaauacaug caagucgagc ggacauuuag gagcuugcuc 60  
 cuaaauguua gcggcgagc ggugaguaac acgugggcaa ccugcccugu agacugggau 120  
 aacaucgaga aaucggugcu aaauaccggau aaucuuaggg auugcauaau ccucuuguaa 180  
 aagauggcuc cggcuauac uacggggaug gcccgcgcg cauuaagcuag uugguaagg 240  
 aacggcuuac caaggcgac augcguagc gaccugagag ggugaucggc cacacuggga 300  
 cugagacacg gccagacuc cuacgggagg cagcaguagg gaaucuuccg caauggacga 360  
 aagucugacg gagcaacgcc gcgugaguga ugaaggguuu cggcucguaa agcucuguug 420  
 uuagggaaga acaagugccg uucaauagg gcggcaccuu gacgguaccu aaccagaaaag 480  
 ccacggcuua cuacgugcca gcagccgcg uaauacguag guggcaagcg uuguccggaa 540  
 uuauugggcg uaaagcgcg gcagggcguc uuuaagucg augugaaaau cucggggcuc 600  
 aaccccgagc ggucauugga aacugggaga cuugaguaca gaagaggaga guggaaaucc 660  
 acguguagcg gugaaaugcg uagauaugug gaggaacacc aguggcgaag gcgacucuc 720

ggucuguaac ugacgcugag gcgcgaaagc guggggagca aacaggauua gauacccugg 780  
 uaguccacgc cguaaacgau gagugcuagg uguuaggggu uucgaugccc uuagugccga 840  
 aguaaacaca uuaagcacuc cgccugggga guacgaccgc aagguugaaa cucaaaggaa 900  
 uugacggggg cccgcacaag caguggagca ugugguuuaa uucgaagcaa cgccaagaac 960  
 cuuaccaggu cuugacaucc uuaugaccuc ccuagagaua gggauuuccc uucgggggaca 1020  
 uaagugacag guggugcaug guugucguca gcucgugucg ugagauguug gguuaagucc 1080  
 cgcaacgagc gcaacccuug aucuuaguug ccagcauuua guugggcacu cuaaggugac 1140  
 ugccggugau aaaccggagg aaggugggga ugacgucaaa ucaucaugcc ccuuauagacc 1200  
 ugggcuacac acgugcuaca auggauggua caaagagcag caaaaccgcg aggucgagcc 1260  
 aaucucauaa agccauucuc aguucggauu guaggcugca acucgccuac augaagccgg 1320  
 aaugcuagu aaucgcggau cagcaugccg cggugaauac guucccgggc cuuguacaca 1380  
 ccgcccguca caccacgaga guuuguaaca cccgaagucg guggaguaac ccuacggga 1440  
 gcuagccgcc uaagguggga cagaugauug gggugaaguc guaacaaggu agccguaucg 1500  
 gaaggugc 1508

<210> 35  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer

<400> 35  
 gtcgccgggg cgcccgctat caattggtaa ctgtatctca gc 42

<210> 36  
 <211> 64  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer

<400> 36  
 gtcgccgggg agctctgatc aggtaccaag cttgtcgacc tgcagaatga ggcagcaaga 60  
 agat 64

<210> 37  
 <211> 61

<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Primer  
  
<400> 37  
gtcggcgcc gctgatcacg taccaagctt gtcgacctgc agaagaggc agcaagaaga 60  
t 61

<210> 38  
<211> 35  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Primer  
  
E <400> 38  
gtcggagctc tatcaattgg taactgtatc tcagc 35

<210> 39  
<211> 35  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Primer  
  
<400> 39  
aacagctgat cagactgat ctttagctt ggcac 35

<210> 40  
<211> 37  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Primer  
  
<400> 40  
aactgcagcc gcggcacatc ataatgggac aaatggg 37

<210> 41  
<211> 45  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Primer  
  
<400> 41

gttgagaaag cggccgcctt ttttctattc tacaatcaca ttatc

45

<210> 42

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 42

gacgacgtac aagcggccgc tcactacgga gaagttcctc catcag

46

<210> 43

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 43

cattctgcag ccgcgga aaa ttccggattt tatgtaagcg g

41

<210> 44

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 44

gttgagaaag cggccgcctt ttttctattc tacaatcaca ttatc

45

<210> 45

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 45

cattctgcag ccgcgga aaa ttccggattt tatgtaagcg g

41

<210> 46

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 46

catcatgcta gctgtaaaaa cggtgcttaa tctcg

35

<210> 47

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 47

cattctgcag ccgcggcagc aagtacaggc ttttatgttg atgg

44

<210> 48

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 48

gacgacgtac aagcggccgc gctatttccc taacatgatg atattttcg

49

<210> 49

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 49

Ala Ser Pro Glu Pro Thr Pro Glu Pro Thr

1

5

10

<210> 50

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 50

cattctgcag ccgcggcatt ttctggaagc gtttcagc

38

<210> 51

<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 51  
cagcagtagc ggccgccact tcctgctggt acatatgc 38

<210> 52  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

*R*  
<400> 52  
cattctgcag ccgcggcaca tcacagtggg ttccatg 37

<210> 53  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 53  
gcgttgagac gcgcggccgc ttattgaaac aactgcttc ttttag 46

<210> 54  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 54  
cattctgcag ccgcggcaag tggacatggg caaatgc 37

<210> 55  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 55  
gcgttgagac gcgcggccgc ttattttttg tatacactaa cgatttc 47